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                         GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:         June  8, 2004, 02:36:13 ; Search time 1292 Seconds
                                          (without alignments)
                                          11249.628 Million cell updates/sec

Title:          US-09-900-448-1
Perfect score:  3186
Sequence:       1 ctctgcagctcagcatggct..........accttttgctgtgttctca 3186

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters:      5991872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_NA:*
                1:  /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                2:  /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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                19:  /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                 SUMMARIES

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Result           Query
  No.    Score   Match Length DB  ID                         Description
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    1     3186   100.0   3186  11  US-09-900-448-1             Sequence 1, Appli
    2   2279.2    71.5  13737  11  US-09-900-448-3             Sequence 3, Appli
    3   1129.8    35.5   1631  15  US-10-125-237-19            Sequence 19, Appl
    4   1129.8    35.5   1631  15  US-10-105-891-19            Sequence 19, Appl
    5    644.8    20.2    861  16  US-10-162-335-87            Sequence 87, Appl
    6    576.8    18.1   1516  15  US-10-175-523-84            Sequence 84, Appl
    7    576.8    18.1   1516  15  US-10-316-253-39            Sequence 39, Appl
    8      427    13.4    488  10  US-09-918-995-30828         Sequence 30828, A
    9      421    13.2    422  10  US-09-918-995-8595          Sequence 8595, Ap
   10      417    13.1    492  10  US-09-918-995-31395         Sequence 31395, A
   11    374.2    11.7    488  10  US-09-918-995-30754         Sequence 30754, A
   12    345.4    10.8    491  10  US-09-918-995-32820         Sequence 32820, A
c  13    313.4     9.8    504  9  US-09-880-107-3166          Sequence 3166, Ap
   14    298.4     9.4    420  9  US-09-960-352-10323         Sequence 10323, A
   15      280     8.8    408  9  US-09-960-352-7040          Sequence 7040, Ap
   16      278     8.7    384  10  US-09-918-995-7738          Sequence 7738, Ap
   17    276.4     8.7    473  10  US-09-918-995-32181         Sequence 32181, A
   18    269.2     8.4    374  9  US-09-960-352-5368          Sequence 5368, Ap
   19    266.8     8.4    383  9  US-09-960-352-6846          Sequence 6846, Ap
   20    264.4     8.3    437  9  US-09-960-352-380           Sequence 380, App
   21    261.8     8.2    405  9  US-09-960-352-445           Sequence 445, App
   22    260.2     8.2    425  9  US-09-960-352-3702          Sequence 3702, Ap
   23      259     8.1    425  9  US-09-960-352-9378          Sequence 9378, Ap
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   25      256     8.0    387  9  US-09-960-352-11316         Sequence 11316, A
   26      256     8.0    422  9  US-09-960-352-7056          Sequence 7056, Ap
   27    255.2     8.0    418  9  US-09-960-352-13395         Sequence 13395, A
   28      255     8.0    373  9  US-09-960-352-2026          Sequence 2026, Ap
   29    254.4     8.0    412  9  US-09-960-352-2507          Sequence 2507, Ap
   30    251.4     7.9    439  9  US-09-960-352-13402         Sequence 13402, A
   31    251.2     7.9    404  9  US-09-960-352-7514          Sequence 7514, Ap
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   34    250.2     7.9    431  9  US-09-960-352-7320          Sequence 7320, Ap
   35    249.8     7.8    399  9  US-09-960-352-457           Sequence 457, App
   36    249.4     7.8    407  9  US-09-960-352-136           Sequence 136, App
   37    249.4     7.8    407  9  US-09-960-352-6107          Sequence 6107, Ap
   38    249.4     7.8    411  9  US-09-960-352-5619          Sequence 5619, Ap
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   40    248.6     7.8    407  9  US-09-960-352-5920          Sequence 5920, Ap
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   44    243.6     7.6    392  9  US-09-960-352-1789          Sequence 1789, Ap
   45    243.2     7.6    384  9  US-09-960-352-9132          Sequence 9132, Ap

                                 ALIGNMENTS

RESULT 1
US-09-900-448-1
; Sequence 1, Application US/09900448
; Publication No. US20030220488A1
; GENERAL INFORMATION:
;  APPLICANT: CECCARDI, Toni et al.
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001272
;  CURRENT APPLICATION NUMBER: US/09/900,448
;  CURRENT FILING DATE:  2001-07-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 3186
;   TYPE: DNA
;   ORGANISM: Human
US-09-900-448-1

  Query Match             100.0%;  Score 3186;  DB 11;  Length 3186;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3186;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCTGCAGCTCAGCATGGCTAGGGTACTGGAGCACCCGTTGCACTGGGGTTGTGGAGCC 60
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Qy         61 TATGCTGGTCTCTGGCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTG 120
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Qy        121 CTGAAGGCGAGACCAAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCT 180
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Qy        181 TTGATGCTACCACCCTGGATGACAATGGAACCATGCTGTTTTTTAAAGGGGAGTTTGTGT 240
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Db          181 TTGATGCTACCACCCTGGATGACAATGGAACCATGCTGTTTTTAAAGGGGAGTTTGTGT 240

Qy          241 GGAAGAGTCACAAATGGACCGGGAGTTAATCTCAGAGAGATGGAAGAATTTCCCCAGCC 300
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Qy          301 CTGTGGATGCTGCATTCCGTCAAGGTCACAACAGTGTCTTTCTGATCAAGGGGGACAAAG 360
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Qy          541 GTACCCACCATGGCCCTGAGTATATGCGCTGTAGCCCACATCTAGTCTTGTCTGCACTGA 600
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Qy          721 CAGTGGATGCTGCCTTTTCCTGGGAAGAAAAACTCTATCTGGTCCAGGGCACCCAGGTAT 780
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Qy          781 ATGTCTTCCTGACAAAGGGAGGCTATACCCTAGTAAGCGGTTATCCGAAGCGGCTGGAGA 840
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Qy          841 AGGAAGTCGGGACCCCTCATGGGATTATCCTGGACTCTGTGGATGCGGCCTTTATCTGCC 900
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Qy          901 CTGGGTCTTCTCGGCTCCATATCATGGCAGGACGGCGGCTGTGGTGGCTGGACCTGAAGT 960
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Qy         1021 TGTGTATGGAAAAGTCCCTTGGCCCTAACTCATGTTCCGCCAATGGTCCCGGCTTGTACC 1080
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Qy         1201 GACATGAGTCTGGCCTGGCCCCACCTCCTAGTTCCTCATAATAAAGACAGATTGCTTCTT 1260
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Qy         1261 CGCTTCTCACTGAGGGGCCTTCTGACATGAGTCTGGCCTGGCCCCACCTCCCCAGTTTCT 1320
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Qy         1321 CATAATAAAGACAGATTGCTTCTTCACTTGAATCAAGGGACCTTGGTCGTGAAACAATCT 1380
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Qy         1621 TGATTCAACTTGCTGGTAGATGGCCACAACCCAGCCGCAAGGCATCAGAAACAACAGGGC 1680
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Qy         1741 TCTGGGGGACCTCAAATTATGGTTCTGGGTGATTCAAGTAACACCACTCATGGCTTGTGT 1800
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Qy         1801 TGCCATGAGTTAGGCATGACAAGTGGAATGAAGTTGAAGTGGGGAAACAGAAATACACCA 1860
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Qy         1861 GCTGTGTGTCAGAGGCAAGCTGGAGAGAGAGAAGAAAGAATGAATGGCACCATGGAGCAC 1920
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Qy         1921 ATTTGCAGAACACAGTCCCTGGGAGTCTTGCTGGAGCCTCAGGAGCTTTGCTGGCACAGA 1980
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1921 ATTTGCAGAACACAGTCCCTGGGAGTCTTGCTGGAGCCTCAGGAGCTTTGCTGGCACAGA 1980

Qy         1981 GGATCTGGCCTACCCAATTAGCCTCCTGGGTATCTGCACCATCTAGACCAGCAAATGTCA 2040
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Qy         2161 CTCAGACAAGGCCCTATTCCTCCACTGCCTTTACAACCCAGCTGAGGTTGGAGGCTGGCT 2220
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Qy         2221 TGTTTCAGCCTCAAAAAATAGCCTGAGTTTCCAGCAGAGGGCCCTTATTCTGAGCTTCCG 2280
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Qy       2581 GGGGACAGTGTCTCAGATTAGGGTCTAACTAGGAAGTTGACTGGAGCTGAGAACAGAGGT 2640
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 CAGCAATAGGAATTTATTGTTCACAATTCTGGAGGCTGGAAAATCCAAGATCAAGGCTCC 3120

Qy       3121 AGCAGGTTCAGTGTCTGCTGAGTGCTTGTTCTGCTTCGAAGATGGCACCTTTTTGCTGTG 3180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 AGCAGGTTCAGTGTCTGCTGAGTGCTTGTTCTGCTTCGAAGATGGCACCTTTTTGCTGTG 3180

Qy       3181 TTCTCA 3186
              ||||||
Db       3181 TTCTCA 3186


RESULT 2
US-09-900-448-3
; Sequence 3, Application US/09900448
; Publication No. US20030220488A1
; GENERAL INFORMATION:
;  APPLICANT: CECCARDI, Toni et al.
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001272
;  CURRENT APPLICATION NUMBER: US/09/900,448
;  CURRENT FILING DATE:  2001-07-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 13737
;   TYPE: DNA
;   ORGANISM: Human
US-09-900-448-3

  Query Match             71.5%;  Score 2279.2;  DB 11;  Length 13737;
  Best Local Similarity   90.9%;  Pred. No. 0;
  Matches 2554;  Conservative    0;  Mismatches    3;  Indels  253;  Gaps    2;

Qy        630 TTCAGTGGACCCACTACTGGCGTCTGGACACCAGCCGGGATGGCTGGCATAGCTGGCCC 689
              | ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10928 TCCACAGGACCCACTACTGGCGTCTGGACACCAGCCGGGATGGCTGGCATAGCTGGCCC 10987

Qy        690 ATTGCTCATCAGTGGCCCCAGGGTCCTTCAGCAGTGGATGCTGCCTTTTCCTGGGAAGAA 749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10988 ATTGCTCATCAGTGGCCCCAGGGTCCTTCAGCAGTGGATGCTGCCTTTTCCTGGGAAGAA 11047

Qy        750 AAACTCTATCTGG----------------------------------------------- 762
              |||||||||||||
Db      11048 AAACTCTATCTGGTCCAGGTGTGTATTGGGGAGAGGCTTGAGGTAGAGACTGGGACAAG 11107

Qy        763 ------------------------------------TCCAGGGCACCCAGGTATATGTCT 786
                                                  ||||||||||||||||||||||||
Db      11108 CATATCCAACTCTGTATTTATTACCATCCTTTGTCCTCCAGGGCACCCAGGTATATGTCT 11167

Qy        787 TCCTGACAAAGGGAGGCTATACCCTAGTAAGCGGTTATCCGAAGCGGCTGGAGAAGGAAG 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11168 TCCTGACAAAGGGAGGCTATACCCTAGTAAGCGGTTATCCGAAGCGGCTGGAGAAGGAAG 11227

Qy        847 TCGGGACCCCTCATGGGATTATCCTGGACTCTGTGGATGCGGCCTTTATCTGCCCTGGGT 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11228 TCGGGACCCCTCATGGGATTATCCTGGACTCTGTGGATGCGGCCTTTATCTGCCCTGGGT 11287

Qy        907 CTTCTCGGCTCCATATCATGG--------------------------------------- 927
              |||||||||||||||||||||
Db      11288 CTTCTCGGCTCCATATCATGGCAGGTGAGGGGCTTCTGGGTGCTTAGAGGGCAGCTTGTT 11347

Qy        928 ------------------------------------------------------------ 927

Db      11348 CTGCTACCTGTCTGTGGCATAGATCCCCACCAGGGCATGAGAAGGCCTAGGTCAGGATCC 11407

Qy        928 ------------------------------------------------------------ 927

Db      11408 CCAGGGCATGAGAAGGCCTAGGTCAGGATCCCCATGACATGGAAGCCATGCTATGTTTGG 11467

Qy        928 -----------CAGGACGGCGGCTGTGGTGGCTGGACCTGAAGTCAGGAGCCCAAGCCAC 976
                         |||||||||||||||||||||||||||||||||||||||||||||||||
Db      11468 TGCCTTCTCCCCAGGACGGCGGCTGTGGTGGCTGGACCTGAAGTCAGGAGCCCAAGCCAC 11527

Qy        977 GTGGACAGAGCTTCCTTGGCCCCATGAGAAGGTAGACGGAGCCTTGTGTATGGAAAAGTC 1036
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11528 GTGGACAGAGCTTCCTTGGCCCCATGAGAAGGTAGACGGAGCCTTGTGTATGGAAAAGTC 11587

Qy       1037 CCTTGGCCCTAACTCATGTTCCGCCAATGGTCCCGGCTTGTACCTCATCCATGGTCCCAA 1096
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11588 CCTTGGCCCTAACTCATGTTCCGCCAATGGTCCCGGCTTGTACCTCATCCATGGTCCCAA 11647

Qy       1097 TTTGTACTGCTACAGTGATGTGGAGAAACTGAATGCAGCCAAGGCCCTTCCGCAACCCCA 1156
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11648 TTTGTACTGCTACAGTGATGTGGAGAAACTGAATGCAGCCAAGGCCCTTCCGCAACCCCA 11707

Qy       1157 GAATGTGACCAGTCTCCTGGGCTGCACTCACTGAGGGGCCTTCTGACATGAGTCTGGCCT 1216
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11708 GAATGTGACCAGTCTCCTGGGCTGCACTCACTGAGGGGCCTTCTGACATGAGTCTGGCCT 11767

Qy       1217 GGCCCCACCTCCTAGTTCCTCATAATAAAGACAGATTGCTTCTTCGCTTCTCACTGAGGG 1276
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11768 GGCCCCACCTCCTAGTTCCTCATAATAAAGACAGATTGCTTCTTCGCTTCTCACTGAGGG 11827

Qy       1277 GCCTTCTGACATGAGTCTGGCCTGGCCCCACCTCCCCAGTTTCTCATAATAAAGACAGAT 1336
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11828 GCCTTCTGACATGAGTCTGGCCTGGCCCCACCTCCCCAGTTTCTCATAATAAAGACAGAT 11887
```

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Qy        1337 TGCTTCTTCACTTGAATCAAGGGACCTTGGTCGTGAAACAATCTTCTTTCTTTGAGTTGA 1396
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       11888 TGCTTCTTCACTTGAATCAAGGGACCTTGGTCGTGAAACAATCTTCTTTCTTTGAGTTGA 11947

Qy        1397 AAAGTTAGCACTTCTCCTTTGAGGGTGTCGAGCTCAAACAAGGCTGTGAGAAACAAGGGA 1456
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       11948 AAAGTTAGCACTTCTCCTTTGAGGGTGTCGAGCTCAAACAAGGCTGTGAGAAACAAGGGA 12007

Qy        1457 GGGGAGCACTAAGGGGCAAACCTATCTCTGCGCAGATGATTCTTAGGTCCAGATCATAAA 1516
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12008 GGGGAGCACTAAGGGGCAAACCTATCTCTGCGCAGATGATTCTTAGGTCCAGATCATAAA 12067

Qy        1517 CTAGCTCTTTGCAGACTATCTACACATAGTGGGGGAAAGAGAACCAGAGTCGGAAGAGG 1576
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12068 CTAGCTCTTTGCAGACTATCTACACATAGTGGGGGAAAGAGAACCAGAGTCGGAAGAGG 12127

Qy        1577 AACAGCTGAGTTTATACAGCAAGTAAGAGGTGGAGCTAGGACTCTGATTCAACTTGCTGG 1636
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12128 AACAGCTGAGTTTATACAGCAAGTAAGAGGTGGAGCTAGGACTCTGATTCAACTTGCTGG 12187

Qy        1637 TAGATGGCCACAACCCAGCCGCAAGGCATCAGAAACAACAGGGCCTGGGGCAACTATGCA 1696
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12188 TAGATGGCCACAACCCAGCCGCAAGGCATCAGAAACAACAGGGCCTGGGGCAACTATGCA 12247

Qy        1697 TGTGCAAAGAGGATTGGCTCAGAGTTGTGGGGTAGGAGGTCCAATCTGGGGGACCTCAAA 1756
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12248 TGTGCAAAGAGGATTGGCTCAGAGTTGTGGGGTAGGAGGTCCAATCTGGGGGACCTCAAA 12307

Qy        1757 TTATGGTTCTGGGTGATTCAAGTAACACCACTCATGGCTTGTGTTGCCATGAGTTAGGCA 1816
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12308 TTATGGTTCTGGGTGATTCAAGTAACACCACTCATGGCTTGTGTTGCCATGAGTTAGGCA 12367

Qy        1817 TGACAAGTGGAATGAAGTTGAAGTGGGGAAACAGAAATACACCAGCTGTGTGTCAGAGGC 1876
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12368 TGACAAGTGGAATGAAGTTGAAGTGGGGAAACAGAAATACACCAGCTGTGTGTCAGAGGC 12427

Qy        1877 AAGCTGGAGAGAGAGAAGAAAGAATGAATGGCACCATGGAGCACATTTGCAGAACACAGT 1936
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12428 AAGCTGGAGAGAGAGAAGAAAGAATGAATGGCACCATGGAGCACATTTGCAGAACACAGT 12487

Qy        1937 CCCTGGGAGTCTTGCTGGAGCCTCAGGAGCTTTGCTGGCACAGAGGATCTGGCCTACCCA 1996
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12488 CCCTGGGAGTCTTGCTGGAGCCTCAGGAGCTTTGCTGGCACAGAGGATCTGGCCTACCCA 12547

Qy        1997 ATTAGCCTCCTGGGTATCTGCACCATCTAGACCAGCAAATGTCACTGGCAAGGAGGTTGC 2056
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12548 ATTAGCCTCCTGGGTATCTGCACCATCTAGACCAGCAAATGTCACTGGCAAGGAGGTTGC 12607

Qy        2057 AGTGCTTGGTTATTTTCTGGTCATAAACTGGTGAAGGCTTTGGGTTCCAAATTTGCTGAC 2116
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12608 AGTGCTTGGTTATTTTCTGGTCATAAACTGGTGAAGGCTTTGGGTTCCAAATTTGCTGAC 12667

Qy        2117 AGCTGTTTAACTGGGAATTGGGCCTAGACTATAGGTAGCTATGTCTCAGACAAGGCCCTA 2176
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12668 AGCTGTTTAACTGGGAATTGGGCCTAGACTATAGGTAGCTATGTCTCAGACAAGGCCCTA 12727

Qy        2177 TTCCTCCACTGCCTTTACAACCCAGCTGAGGTTGGAGGCTGGCTTGTTTCAGCCTCAAAA 2236
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12728 TTCCTCCACTGCCTTTACAACCCAGCTGAGGTTGGAGGCTGGCTTGTTTCAGCCTCAAAA 12787

Qy        2237 AATAGCCTGAGTTTCCAGCAGAGGGCCCTTATTCTGAGCTTCCGTGTCCTAGCCTCATTT 2296
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12788 AATAGCCTGAGTTTCCAGCAGAGGGCCCTTATTCTGAGCTTCCGTGTCCTAGCCTCATTT 12847

Qy        2297 TCCTTTCCTGTAAAATAGACACAATGCCACCCACCTTCCAGTGACAATGAATATAGACTC 2356
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12848 TCCTTTCCTGTAAAATAGACACAATGCCACCCACCTTCCAGTGACAATGAATATAGACTC 12907

Qy        2357 AAACCCATCCCTTGAACTGTCTTGGGAAGGGGCTCTGGACGTAGACCCAGACTGTGGCTC 2416
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12908 AAACCCATCCCTTGAACTGTCTTGGGAAGGGGCTCTGGACGTAGACCCAGACTGTGGCTC 12967

Qy        2417 ATGGCCTCATGTGATCTGGAGTCAGCCCCTCCCAACCTGTCAGCCATTTGCTCCGTAGGA 2476
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       12968 ATGGCCTCATGTGATCTGGAGTCAGCCCCTCCCAACCTGTCAGCCATTTGCTCCGTAGGA 13027

Qy        2477 CTTTGATGGGTAGAGTAGTAGCTAACAAGCTCTGACTGTCACACAAGGCTTTGTACTGGG 2536
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       13028 CTTTGATGGGTAGAGTAGTAGCTAACAAGCTCTGACTGTCACACAAGGCTTTGTACTGGG 13087

Qy        2537 AGGCCAGGCTATAGAGTGGCTCCAGCTTAAAGGGCTGGAGCTGGGGGACAGTGTCTCAG 2596
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       13088 AGGCCAGGCTATAGAGTGGCTCCAGCTTAAAGGGCTGGAGCTGGGGGACAGTGTCTCAG 13147

Qy        2597 ATTAGGGTCTAACTAGGAAGTTGACTGGAGCTGAGAACAGAGGTTAGGGGCCAAGCAGCA 2656
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       13148 ATTAGGGTCTAACTAGGAAGTTGACTGGAGCTGAGAACAGAGGTTAGGGGCCAAGCAGCA 13207

Qy        2657 GGGTTGTGGGTCTACTCCTTAGGAGCACCTTGAGCTTTACTTTTCATTCCTAATGGTGTC 2716
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       13208 GGGTTGTGGGTCTACTCCTTAGGAGCACCTTGAGCTTTACTTTTCATTCCTAATGGTGTC 13267

Qy        2717 TTGGATGGCTACCCTCACGGGGTTGGCTGCTAGTCTAAGGGGTGGAGACAAGGACAGAGT 2776
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       13268 TTGGATGGCTACCCTCACGGGGTTGGCTGCTAGTCTAAGGGGTGGAGACAAGGACAGAGT 13327

Qy        2777 TTCAGGTCTGGTCCTTATCAAGTTCATGCACTACACTTGGGACCACTGCTGCATCATGCC 2836
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       13328 TTCAGGTCTGGTCCTTATCAAGTTCATGCACTACACTTGGGACCACTGCTGCATCATGCC 13387

Qy        2837 AGGGAGCCTAGAGGTGTCTAAACAGTTATCCAACAACTGTGATACCCAAGGTTAACTTTC 2896
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       13388 AGGGAGCCTAGAGGTGTCTAAACAGTTATCCAACAACTGTGATACCCAAGGTTAACTTTC 13447

Qy        2897 TCTTGTTTTCAGAGGCAGGGAGTACTAAGTCTCCCCTTTCTCCTTTCCTCCCACGTGTTC 2956
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       13448 TCTTGTTTTCAGAGGCAGGGAGTACTAAGTCTCCCCTTTCTCCTTTCCTCCCACGTGTTC 13507

Qy        2957 TCTTGCAGGGAATCCTCTAGCTTGTCTCCAGGGAACTCCCAGAAATGGTTTGTTTCAGTC 3016
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       13508 TCTTGCAGGGAATCCTCTAGCTTGTCTCCAGGGAACTCCCAGAAATGGTTTGTTTCAGTC 13567

Qy        3017 AGTTTAGGCTGCTATAAGAGAATATCTTAGAGTGGGTAATCTATCAGCAATAGGAATTTA 3076
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       13568 AGTTTAGGCTGCTATAAGAGAATATCTTAGAGTGGGTAATCTATCAGCAATAGGAATTTA 13627

Qy        3077 TTGTTCACAATTCTGGAGGCTGGAAAATCCAAGATCAAGGCTCCAGCAGGTTCAGTGTCT 3136
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       13628 TTGTTCACAATTCTGGAGGCTGGAAAATCCAAGATCAAGGCTCCAGCAGGTTCAGTGTCT 13687

Qy        3137 GCTGAGTGCTTGTTCTGCTTCGAAGATGGCACCTTTTTGCTGTGTTCTCA 3186
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       13688 GCTGAGTGCTTGTTCTGCTTCGAAGATGGCACCTTTTTGCTGTGTTCTCA 13737


RESULT 3
US-10-125-237-19
; Sequence 19, Application US/10125237
; Publication No. US20030022329A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: No. US20030022329A1el Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 791CIP2ADIV
;  CURRENT APPLICATION NUMBER: US/10/125,237
;  CURRENT FILING DATE:  2002-04-17
;  PRIOR APPLICATION NUMBER: 09/668,317
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: 09/552,929
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 91
;  SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 19
;   LENGTH: 1631
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (71)..(1459)
US-10-125-237-19

  Query Match             35.5%;  Score 1129.8;  DB 15;  Length 1631;
  Best Local Similarity   86.3%;  Pred. No. 0;
  Matches 1354;  Conservative    0;  Mismatches    2;  Indels  213;  Gaps    1;

Qy        1 CTCTGCAGCTCAGCATGGCTAGGGTACTGGGAGCACCCGTTGCACTGGGGTTGTGGAGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       57 CTCTGCAGCTCAGCATGGCTAGGGTACTGGGAGCACCCGTTGCACTGGGGTTGTGGAGCC 116

Qy       61 TATGCTGGTCTCTGGCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      117 TATGCTGGTCTCTGGCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTG 176

Qy      121 CTGAAGGCGAGACCAAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCT 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      177 CTGAAGGCGAGACCAAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCT 236

Qy      181 TTGATGCTACCACCCTGGATGACAATGGAACCATGCTGTTTTTTAAAGGGGAGTTTGTGT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      237 TTGATGCTACCACCCTGGATGACAATGGAACCATGCTGTTTTTTAAAGGGGAGTTTGTGT 296

Qy      241 GGAAGAGTCACAAATGGGACCGGGAGTTAATCTCAGAGAGATGGAAGAATTTCCCCAGCC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      297 GGAAGAGTCACAAATGGGACCGGGAGTTAATCTCAGAGAGATGGAAGAATTTCCCCAGCC 356

Qy      301 CTGTGGATGCTGCATTCCGTCAAGGTCACAACAGTGTCTTTCTGATCAAGGGGGACAAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      357 CTGTGGATGCTGCATTCCGTCAAGGTCACAACAGTGTCTTTCTGATCAAGGGGGACAAAG 416

Qy      361 TCTGGGTATACCCTCCTGAAAAGAAGGAGAAAGGATACCCAAAGTTGCTCCAAGATGAAT 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      417 TCTGGGTATACCCTCCTGAAAAGAAGGAGAAAGGATACCCAAAGTTGCTCCAAGATGAAT 476

Qy      421 TTCCTGGAATCCCATCCCCACTGGATGCAGCTGTGGAATGTCACCGTGGAGAATGTCAAG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      477 TTCCTGGAATCCCATCCCCACTGGATGCAGCTGTGGAATGTCACCGTGGAGAATGTCAAG 536

Qy      481 CTGAAGGCGTCCTCTTCTTCCA-------------------------------------- 502
            ||||||||||||||||||||||
Db      537 CTGAAGGCGTCCTCTTCTTCCAAGGTGACCGCGAGTGGTTCTGGGACTTGGCTACGGGAA 596

Qy      503 ------------------------------------------------------------ 502

Db      597 CCATGAAGGAGCGTTCCTGGCCAGCTGTTGGGAACTGCTCCTCTGCCCTGAGATGGCTGG 656

Qy      503 ------------------------------------------------------------ 502

Db      657 GCCGCTACTACTGCTTCCAGGGTAACCAATTCCTGCGCTTCGACCCTGTCAGGGGAGAGG 716

Qy      503 -------------------------------------------------------AGGCC 507
                                                                   |||||
Db      717 TGCCTCCCAGGTACCCGCGGGATGTCCGAGACTACTTCATGCCCTGCCCTGGCAGAGGCC 776

Qy      508 ATGGACACAGGAATGGGACTGGCCATGGGAACAGTACCCACCATGGCCCTGAGTATATGC 567
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      777 ATGGACACAGGAATGGGACTGGCCATGGGAACAGTACCCACCATGGCCCTGAGTATATGC 836

Qy      568 GCTGTAGCCCACATCTAGTCTTGTCTGCACTGACGTCTGACAACCATGGTGCCACCTATG 627
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      837 GCTGTAGCCCACATCTAGTCTTGTCTGCACTGACGTCTGACAACCATGGTGCCACCTATG 896

Qy      628 CCTTCAGTGGGACCCACTACTGGCGTCTGGACACCAGCCGGGATGGCTGGCATAGCTGGC 687
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      897 CCTTCAGTGGGACCCACTACTGGCGTCTGGACACCAGCCGGGATGGCTGGCATAGCTGGC 956

Qy      688 CCATTGCTCATCAGTGGCCCCAGGGTCCTTCAGCAGTGGATGCTGCCTTTTCCTGGGAAG 747
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      957 CCATTGCTCATCAGTGGCCCCAGGGTCCTTCAGCAGTGGATGCTGCCTTTTCCTGGGAAG 1016

Qy      748 AAAAACTCTATCTGGTCCAGGGCACCCAGGTATATGTCTTCCTGACAAAGGGAGGCTATA 807
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1017 AAAAACTCTATCTGGTCCAGGGCACCCAGGTATATGTCTTCCTGACAAAGGGAGGCTATA 1076

Qy      808 CCCTAGTAAGCGGTTATCCGAAGCGGCTGGAGAAGGAAGTCGGGACCCCTCATGGGATTA 867
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1077 CCCTAGTAAGCGGTTATCCGAAGCGGCTGGAGAAGGAAGTCGGGACCCCTCATGGGATTA 1136

Qy      868 TCCTGGACTCTGTGGATGCGGCCTTTATCTGCCCTGGGTCTTCTCGGCTCCATATCATGG 927
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1137 TCCTGGACTCTGTGGATGCGGCCTTTATCTGCCCTGGGTCTTCTCGGCTCCATATCATGG 1196

Qy      928 CAGGACGGCGGCTGTGGTGGCTGGACCTGAAGTCAGGAGCCCAAGCCACGTGGACAGAGC 987
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1197 CAGGACGGCGGCTGTGGTGGCTGGACCTGAAGTCAGGAGCCCAAGCCACGTGGACAGAGC 1256

Qy      988 TTCCTTGGCCCCATGAGAAGGTAGACGGAGCCTTGTGTATGGAAAAGTCCCTTGGCCCTA 1047
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1257 TTCCTTGGCCCCATGAGAAGGTAGACGGAGCCTTGTGTATGGAAAAGTCCCTTGGCCCTA 1316

Qy     1048 ACTCATGTTCCGCCAATGGTCCCGGCTTGTACCTCATCCATGGTCCCAATTTGTACTGCT 1107
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1317 ACTCATGTTCCGCCAATGGTCCCGGCTTGTACCTCATCCATGGTCCCAATTTGTACTGCT 1376

Qy     1108 ACAGTGATGTGGAGAAACTGAATGCAGCCAAGGCCCTTCCGCAACCCCAGAATGTGACCA 1167
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1377 ACAGTGATGTGGAGAAACTGAATGCAGCCAAGGCCCTTCCGCAACCCCAGAATGTGACCA 1436

Qy     1168 GTCTCCTGGGCTGCACTCACTGAGGGGCCTTCTGACATGAGTCTGGCCTGGCCCCACCTC 1227
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1437 GTCTCCTGGGCTGCACTCACTGAGGGGCCTTCTGACATGAGTCTGGCCTGGCCCCACCTC 1496

Qy     1228 CTAGTTCCTCATAATAAAGACAGATTGCTTCTTCGCTTCTCACTGAGGGGCCTTCTGACA 1287
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1497 CTAGTTCCTCATAATAAAGACAGATTGCTTCTTCGCTTCTCACTGAGGGGCCTTCTGACA 1556

Qy     1288 TGAGTCTGGCCTGGCCCCACCTCCCCAGTTTCTCATAATAAAGACAGATTGCTTCTTCAC 1347
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1557 TGAGTCTGGCCTGGCCCCACCTCCCCAGTTTCTCATAATAAAGACAGATTGCTTCTTCAC 1616

Qy     1348 TTGAATCAA 1356
            |||||  ||
Db     1617 TTGAAAAAA 1625


RESULT 4
US-10-105-891-19
; Sequence 19, Application US/10105891
; Publication No. US20030073099A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: No. US20030073099A1el Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 791CIP2A
;  CURRENT APPLICATION NUMBER: US/10/105,891
;  CURRENT FILING DATE:  2002-03-25
;  PRIOR APPLICATION NUMBER: 09/668,317
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: 09/552,929
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 91
;  SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 19
;   LENGTH: 1631
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (71)..(1459)
US-10-105-891-19

  Query Match             35.5%;  Score 1129.8;  DB 15;  Length 1631;
  Best Local Similarity   86.3%;  Pred. No. 0;
  Matches 1354;  Conservative    0;  Mismatches    2;  Indels  213;  Gaps    1;

Qy          1 CTCTGCAGCTCAGCATGGCTAGGGTACTGGGAGCACCCGTTGCACTGGGGTTGTGGAGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         57 CTCTGCAGCTCAGCATGGCTAGGGTACTGGGAGCACCCGTTGCACTGGGGTTGTGGAGCC 116

Qy         61 TATGCTGGTCTCTGGCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 TATGCTGGTCTCTGGCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTG 176

Qy        121 CTGAAGGCGAGACCAAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        177 CTGAAGGCGAGACCAAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCT 236

Qy        181 TTGATGCTACCACCCTGGATGACAATGGAACCATGCTGTTTTTTAAAGGGGAGTTTGTGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 TTGATGCTACCACCCTGGATGACAATGGAACCATGCTGTTTTTTAAAGGGGAGTTTGTGT 296

Qy        241 GGAAGAGTCACAAATGGGACCGGGAGTTAATCTCAGAGAGATGGAAGAATTTCCCCAGCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 GGAAGAGTCACAAATGGGACCGGGAGTTAATCTCAGAGAGATGGAAGAATTTCCCCAGCC 356

Qy        301 CTGTGGATGCTGCATTCCGTCAAGGTCACAACAGTGTCTTTCTGATCAAGGGGGACAAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 CTGTGGATGCTGCATTCCGTCAAGGTCACAACAGTGTCTTTCTGATCAAGGGGGACAAAG 416

Qy        361 TCTGGGTATACCCTCCTGAAAAGAAGGAGAAAGGATACCCAAAGTTGCTCCAAGATGAAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 TCTGGGTATACCCTCCTGAAAAGAAGGAGAAAGGATACCCAAAGTTGCTCCAAGATGAAT 476

Qy        421 TTCCTGGAATCCCATCCCCACTGGATGCAGCTGTGGAATGTCACCGTGGAGAATGTCAAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 TTCCTGGAATCCCATCCCCACTGGATGCAGCTGTGGAATGTCACCGTGGAGAATGTCAAG 536

Qy        481 CTGAAGGCGTCCTCTTCTTCCA-------------------------------------- 502
              ||||||||||||||||||||||
Db        537 CTGAAGGCGTCCTCTTCTTCCAAGGTGACCGCGAGTGGTTCTGGGACTTGGCTACGGGAA 596

Qy        503 ------------------------------------------------------------ 502

Db        597 CCATGAAGGAGCGTTCCTGGCCAGCTGTTGGGAACTGCTCCTCTGCCCTGAGATGGCTGG 656

Qy        503 ------------------------------------------------------------ 502

Db        657 GCCGCTACTACTGCTTCCAGGGTAACCAATTCCTGCGCTTCGACCCTGTCAGGGGAGAGG 716

Qy        503 -------------------------------------------------------AGGCC 507
                                                                     |||||
Db        717 TGCCTCCCAGGTACCCGCGGGATGTCCGAGACTACTTCATGCCCTGCCCTGGCAGAGGCC 776

Qy        508 ATGGACACAGGAATGGGACTGGCCATGGGAACAGTACCCACCATGGCCCTGAGTATATGC 567
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        777 ATGGACACAGGAATGGGACTGGCCATGGGAACAGTACCCACCATGGCCCTGAGTATATGC 836

Qy        568 GCTGTAGCCCACATCTAGTCTTGTCTGCACTGACGTCTGACAACCATGGTGCCACCTATG 627
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        837 GCTGTAGCCCACATCTAGTCTTGTCTGCACTGACGTCTGACAACCATGGTGCCACCTATG 896

Qy        628 CCTTCAGTGGGACCCACTACTGGCGTCTGGACACCAGCCGGGATGGCTGGCATAGCTGGC 687
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        897 CCTTCAGTGGGACCCACTACTGGCGTCTGGACACCAGCCGGGATGGCTGGCATAGCTGGC 956

Qy        688 CCATTGCTCATCAGTGGCCCCAGGGTCCTTCAGCAGTGGATGCTGCCTTTTCCTGGGAAG 747
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        957 CCATTGCTCATCAGTGGCCCCAGGGTCCTTCAGCAGTGGATGCTGCCTTTTCCTGGGAAG 1016

Qy        748 AAAAACTCTATCTGGTCCAGGGCACCCAGGTATATGTCTTCCTGACAAAGGGAGGCTATA 807
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1017 AAAAACTCTATCTGGTCCAGGGCACCCAGGTATATGTCTTCCTGACAAAGGGAGGCTATA 1076

Qy        808 CCCTAGTAAGCGGTTATCCGAAGCGGCTGGAGAAGGAAGTCGGGACCCCTCATGGGATTA 867
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1077 CCCTAGTAAGCGGTTATCCGAAGCGGCTGGAGAAGGAAGTCGGGACCCCTCATGGGATTA 1136

Qy        868 TCCTGGACTCTGTGGATGCGGCCTTTATCTGCCCTGGGTCTTCTCGGCTCCATATCATGG 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1137 TCCTGGACTCTGTGGATGCGGCCTTTATCTGCCCTGGGTCTTCTCGGCTCCATATCATGG 1196

Qy        928 CAGGACGGCGGCTGTGGTGGCTGGACCTGAAGTCAGGAGCCCAAGCCACGTGGACAGAGC 987
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1197 CAGGACGGCGGCTGTGGTGGCTGGACCTGAAGTCAGGAGCCCAAGCCACGTGGACAGAGC 1256

Qy        988 TTCCTTGGCCCCATGAGAAGGTAGACGGAGCCTTGTGTATGGAAAAGTCCCTTGGCCCTA 1047
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1257 TTCCTTGGCCCCATGAGAAGGTAGACGGAGCCTTGTGTATGGAAAAGTCCCTTGGCCCTA 1316

Qy       1048 ACTCATGTTCCGCCAATGGTCCCGGCTTGTACCTCATCCATGGTCCCAATTTGTACTGCT 1107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1317 ACTCATGTTCCGCCAATGGTCCCGGCTTGTACCTCATCCATGGTCCCAATTTGTACTGCT 1376

Qy       1108 ACAGTGATGTGGAGAAACTGAATGCAGCCAAGGCCCTTCCGCAACCCCAGAATGTGACCA 1167
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1377 ACAGTGATGTGGAGAAACTGAATGCAGCCAAGGCCCTTCCGCAACCCCAGAATGTGACCA 1436

Qy       1168 GTCTCCTGGGCTGCACTCACTGAGGGGCCTTCTGACATGAGTCTGGCCTGGCCCCACCTC 1227
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1437 GTCTCCTGGGCTGCACTCACTGAGGGGCCTTCTGACATGAGTCTGGCCTGGCCCCACCTC 1496

Qy       1228 CTAGTTCCTCATAATAAAGACAGATTGCTTCTTCGCTTCTCACTGAGGGGCCTTCTGACA 1287
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1497 CTAGTTCCTCATAATAAAGACAGATTGCTTCTTCGCTTCTCACTGAGGGGCCTTCTGACA 1556

Qy       1288 TGAGTCTGGCCTGGCCCCACCTCCCCAGTTTCTCATAATAAAGACAGATTGCTTCTTCAC 1347
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1557 TGAGTCTGGCCTGGCCCCACCTCCCCAGTTTCTCATAATAAAGACAGATTGCTTCTTCAC 1616

Qy       1348 TTGAATCAA 1356
              |||||  ||
Db       1617 TTGAAAAAA 1625


RESULT 5
US-10-162-335-87
; Sequence 87, Application US/10162335
; Publication No. US20040009480A1
; GENERAL INFORMATION:
;  APPLICANT: Anderson, David W.
;  APPLICANT:  Baumgartner, Jason C.
;  APPLICANT:  Boldog, Ferenc L.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Hjalt, Tord
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Li, Li
;  APPLICANT:  MacDougall, John R.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Pena, Carol E. A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Stone, David J.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Vernet, Corine A. M.
;  APPLICANT:  Voss, Edward Z.
;  APPLICANT:  Zerhusen, Bryan D.
;  TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
;  FILE REFERENCE: 21402-377 B
;  CURRENT APPLICATION NUMBER: US/10/162,335
;  CURRENT FILING DATE:  2002-10-01
;  PRIOR APPLICATION NUMBER: 60/295,607
;  PRIOR FILING DATE: 2001-06-04
;  PRIOR APPLICATION NUMBER: 60/295,661
;  PRIOR FILING DATE: 2001-06-04
;  PRIOR APPLICATION NUMBER: 60/296,404
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: 60/296,418
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: 60/297,414
;  PRIOR FILING DATE: 2001-06-11
;  PRIOR APPLICATION NUMBER: 60/297,567
;  PRIOR FILING DATE: 2001-06-12
;  PRIOR APPLICATION NUMBER: 60/298,285
;  PRIOR FILING DATE: 2001-06-14
;  PRIOR APPLICATION NUMBER: 60/298,556
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/299,949
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/300,883
;  PRIOR FILING DATE: 2001-06-26
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 201
; SEQ ID NO 87
;   LENGTH: 861
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (10)..(775)
US-10-162-335-87

  Query Match             20.2%;  Score 644.8;  DB 16;  Length 861;
  Best Local Similarity   96.1%;  Pred. No. 6.6e-204;
  Matches  661;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy        587 CTTGTCTGCACTGACGTCTGACAACCATGGTGCCACCTATGCCTTCAGTGGGACCCACTA 646
              |||   |||    ||    ||  || ||||  |||        || |  |||||||||||
Db        174 CTTTGATGCTACCACCCTGGATGACAATGGAACCATGCTGTTTTTTAAAGGGACCCACTA 233

Qy        647 CTGGCGTCTGGACACCAGCCGGGATGGCTGGCATAGCTGGCCCATTGCTCATCAGTGGCC 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 CTGGCGTCTGGACACCAGCCGGGATGGCTGGCATAGCTGGCCCATTGCTCATCAGTGGCC 293

Qy        707 CCAGGGTCCTTCAGCAGTGGATGCTGCCTTTTCCTGGGAAGAAAAACTCTATCTGGTCCA 766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 CCAGGGTCCTTCAGCAGTGGATGCTGCCTTTTCCTGGGAAGAAAAACTCTATCTGGTCCA 353

Qy        767 GGGCACCCAGGTATATGTCTTCCTGACAAAGGGAGGCTATACCCTAGTAAGCGGTTATCC 826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 GGGCACCCAGGTATATGTCTTCCTGACAAAGGGAGGCTATACCCTAGTAAGCGGTTATCC 413

Qy        827 GAAGCGGCTGGAGAAGGAAGTCGGGACCCCTCATGGGATTATCCTGGACTCTGTGGATGC 886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GAAGCGGCTGGAGAAGGAAGTCGGGACCCCTCATGGGATTATCCTGGACTCTGTGGATGC 473

Qy        887 GGCCTTTATCTGCCCTGGGTCTTCTCGGCTCCATATCATGGCAGGACGGCGGCTGTGGTG 946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 GGCCTTTATCTGCCCTGGGTCTTCTCGGCTCCATATCATGGCAGGACGGCGGCTGTGGTG 533

Qy        947 GCTGGACCTGAAGTCAGGAGCCCAAGCCACGTGGACAGAGCTTCCTTGGCCCCATGAGAA 1006
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 GCTGGACCTGAAGTCAGGAGCCCAAGCCACGTGGACAGAGCTTCCTTGGCCCCATGAGAA 593

Qy       1007 GGTAGACGGAGCCTTGTGTATGGAAAAGTCCCTTGGCCCTAACTCATGTTCCGCCAATGG 1066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 GGTAGACGGAGCCTTGTGTATGGAAAAGTCCCTTGGCCCTAACTCATGTTCCGCCAATGG 653

Qy       1067 TCCCGGCTTGTACCTCATCCATGGTCCCAATTTGTACTGCTACAGTGATGTGGAGAAACT 1126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 TCCCGGCTTGTACCTCATCCATGGTCCCAATTTGTACTGCTACAGTGATGTGGAGAAACT 713

Qy       1127 GAATGCAGCCAAGGCCCTTCCGCAACCCCAGAATGTGACCAGTCTCCTGGGCTGCACTCA 1186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 GAATGCAGCCAAGGCCCTTCCGCAACCCCAGAATGTGACCAGTCTCCTGGGCTGCACTCA 773

Qy       1187 CTGAGGGGCCTTCTGACATGAGTCTGGCCTGGCCCCACCTCCTAGTTCCTCATAATAAAG 1246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 CTGAGGGGCCTTCTGACATGAGTCTGGCCTGGCCCCACCTCCTAGTTCCTCATAATAAAG 833

Qy       1247 ACAGATTGCTTCTTCGCTTCTCACTGAG 1274
              ||||||||||||||||||||||||||||
Db        834 ACAGATTGCTTCTTCGCTTCTCACTGAG 861


RESULT 6
US-10-175-523-84
; Sequence 84, Application US/10175523
; Publication No. US20030096264A1
; GENERAL INFORMATION:
;  APPLICANT: Brockman, Jeffrey
;  APPLICANT:  Evans, David
;  APPLICANT:  Hook, Derek
;  APPLICANT:  Klimczak, Leszek
;  APPLICANT:  Laeng, Pascal
;  APPLICANT:  Palfreyman, Michael
;  APPLICANT:  Rajan, Prithi
;  TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
;  FILE REFERENCE: 3235/1J795-US3
;  CURRENT APPLICATION NUMBER: US/10/175,523
;  CURRENT FILING DATE:  2002-06-18
;  PRIOR APPLICATION NUMBER: US 60/299,151
;  PRIOR FILING DATE: 2001-06-18
;  PRIOR APPLICATION NUMBER: US 60/317,828
;  PRIOR FILING DATE: 2001-09-07
;  PRIOR APPLICATION NUMBER: US 60/325,150
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US 60/333,047
;  PRIOR FILING DATE: 2001-11-14
;  PRIOR APPLICATION NUMBER: US 60/349,936
;  PRIOR FILING DATE: 2002-01-18
;  PRIOR APPLICATION NUMBER: US 60/361,834
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
;   LENGTH: 1516
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-175-523-84

  Query Match             18.1%;  Score 576.8;  DB 15;  Length 1516;
  Best Local Similarity   67.3%;  Pred. No. 5.3e-181;
  Matches  999;  Conservative    0;  Mismatches  257;  Indels  228;  Gaps    4;

Qy          1 CTCTGCAGCTCAGCATGGCTAGGGTACTGGGAGCACCCGTTGCACTGGGGTTGTGGAGCC 60
              || ||||||||  ||||||||||  | | | |||||    |   ||||  |||  | |||
Db         41 CTTTGCAGCTCGCCATGGCTAGGACAGTAGTAGCACTAAATATCCTGGTATTGCTGGGCC 100
```

```
Qy         61 TATGCTGGTCTCTGGCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTG 120
Db        101 TGTGCTGGTCCCTGGCTGTTGCCAACCCTCTTCCTGCTGCCCATGAGACTGTTGCTAAAG 160

Qy        121 CTGAAGGCGAGACCAAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCT 180
Db        161 GTGAAAATGGGACCAAGCCAGACTCAGATGTAATCGAACACTGCTCAGATGCCTGGAGCT 220

Qy        181 TTGATGCTACCACCCTGGATGACAATGGAACCATGCTGTTTTTAAAGGGGAGTTTGTGT 240
Db        221 TTGACGCTACCACCATGGATCACAATGGACCATGCTGTTCTTTAAAGGGGAGTTTGTGT 280

Qy        241 GGAAGAGTCACAAATGGGACCGGGAGTTAATCTCAGAGAGATGGAAGAATTTCCCCAGCC 300
Db        281 GGAGGGGTCACTCAGGGATCCGGGAGTTAATCTCAGAGAGGTGGAAGAATCCCGTCACCT 340

Qy        301 CTGTGGATGCTGCATTCCGTCAAGGTCACAACAGTGTCTTTCTGATCAAGGGGGACAAAG 360
Db        341 CAGTGGATGCTGCATTCCGT---GGTCCTGACAGTGTCTTCCTGATCAAGGAAGACAAAG 397

Qy        361 TCTGGGTATACCCTCCTGAAAAGAAGGAGAAAGGATACCCAAAGTTGCTCCAAGATGAAT 420
Db        398 TCTGGGTGTATCCTCCTGAAAAGAAAGAGAACGGGTATCCAAAGTTGTTCCAAGAAGAGT 457

Qy        421 TTCCTGGAATCCCATCCCCACTGGATGCAGCTGTGGAATGTCACCGTGGAGAATGTCAAG 480
Db        458 CTCCTGGAATCCCATACCCACCAGACGCAGCTGTGGAATGCCACCGTGGAGAATGCCAGA 517

Qy        481 CTGAAGGCGTCCTCTTCTTCCAAGGCCA-------------------------------- 508
Db        518 GTGAAGGTGTCCTCTTCTTCCAAGGTAACCGCAAGTGGTTCTGGGACTTTGCCACAAGAA 577

Qy        509 ------------------------------------------------------------ 508
Db        578 CCCAAAAGGAACGTTCCTGGCCTGCTGTTGGGAATTGCACTGCGGCCTTGAGGTGGCTTG 637

Qy        509 ------------------------------------------------------------ 508
Db        638 AACGCTACTACTGCTTCCAGGGTAACAAGTTCCTGAGATTTAACCCCGTCACAGGAGAGG 697

Qy        509 ------------------------------------------------------------ 508
Db        698 TGCCTCCCAGATACCCTCTGGATGCCCGTGACTACTTCATATCCTGCCCTGGCAGAGGCC 757

Qy        509 ----TGGACACAGGAATGGGACTGGCCATGGGAACAGTACCCACCATGGCCCTGAGTATA 564
Db        758 ATGGTAAACTAAGAAATGGAACTGCTCATGGGAATAGCACCCA------TCCTATGCATT 811

Qy        565 TGCGCTGTAGCCCACATCTAGTCTTGTCTGCACTGACGTCTGACAACCATGGTGCCACCT 624
Db        812 CGCGTTGTAACGCAGATCCTGGCCTGTCTGCACTGCTGTCTGACCATCGAGGTGCCACCT 871

Qy        625 ATGCCTTCAGTGGGACCCACTACTGGCGTCTGGACACCAGCCGGGATGGCTGGCATAGCT 684
Db        872 ATGCCTTCAGTGGCTCCCACTACTGGCGTCTGGACTCCAGCCGTGATGGTGGCATAGCT 931

Qy        685 GGCCCATTGCTCATCAGTGGCCCCAGGGTCCTTCAGCAGTGGATGCTGCCTTTTCCTGGG 744
Db        932 GGCCCATTGCTCATCACTGGCCCCAGGGTCCTTCAGCAGTAGATGCTGCCTTTTCCTGGG 991

Qy        745 AAGAAAAACTCTATCTGGTCCAGGGCACCCAGGTATATGTCTTCCTGACAAAGGGAGGCT 804
Db        992 ATGAGAAAGTCTATCTGATCCAGGGCACTCAAGTATATGTCTTCCTGACGAAGGGGGGCA 1051

Qy        805 ATACCCTAGTAAGCGGTTATCCGAAGCGGCTGGAGAAGGAAGTCGGGACCCCTCATGGGA 864
Db       1052 ATAACCTAGTAAGTGGTTATCCAAAGCGGCTGGAGAAGGAACTTGGGAGCCCTCCCGGGA 1111

Qy        865 TTATCCTGGACTCTGTGGATGCGGCCTTTATCTGCCCTGGGTCTTCTCGGCTCCATATCA 924
Db       1112 TCAGCCTTGATACCATAGATGCAGCCTTTTCCTGCCCTGGTTCTTCCAAGCTCTACGTCA 1171

Qy        925 TGGCAGGACGGCGGCTGTGGTGGCTGGACCTGAAGTCAGGAGCCCAAGCCACGTGGACAG 984
Db       1172 CATCAGGACGGCGGCTTTGGTGGCTGGACCTGAAGTCAGGAGCCCAGGCGACATGGGCAG 1231

Qy        985 AGCTTCCTTGGCCCCATGAGAAGGTAGACGGAGCCTTGTGTATGGAAAAGTCCCTTGGCC 1044
Db       1232 AGCTTTCCTGGCCCCATGAGAAAGTTGATGGTGCCCTGTGTTTGGAAAAGTCCCTTGGTC 1291

Qy       1045 CTAACTCATGTTCCGCCAATGGTCCCGGCTTGTACCTCATCCATGGTCCCAATTTGTACT 1104
Db       1292 CCTACTCATGCTCTTCCAATGGTCCCAACTTGTTCTTTATCCATGGCCCAATTTATACT 1351

Qy       1105 GCTACAGTGATGTGGAGAAACTGAATGCAGCCAAGGCCCTTCCGCAACCCCAGAATGTGA 1164
Db       1352 GCTATAGCAGTATAGACAAACTGAATGCAGCCAAGAGTCTGCCTCAGCCCCAGAAAGTGA 1411

Qy       1165 CCAGTCTCCTGGGCTGCACTCACTGAGGGGCC---TTCTGACATGAGTCTGGCCTGGCCC 1221
Db       1412 ACAGCATCCTTGGCTGCAGTCAATAAAAAGCCCTGATGGAATTAGCCCAGCCCACCCCA 1471

Qy       1222 CACCTCCTAGTTCCTCATAATAAAGACAGATTGCTTCTTCGCTT 1265
Db       1472 CCTCTCCATTTCCATTCTAATAAAACCAGATGGTTTCTTCACAT 1515


RESULT 7
US-10-316-253-39
; Sequence 39, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
;  APPLICANT: The Procter & Gamble Company
;  APPLICANT:  Peters, Kevin
;  APPLICANT:  Thompson, Larry
;  APPLICANT:  Wang, Feng
;  APPLICANT:  Greis, Kenneth
;  TITLE OF INVENTION: Angiogenesis Modulating Proteins
;  FILE REFERENCE: 8865M
;  CURRENT APPLICATION NUMBER: US/10/316,253
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: US 60/355,295
;  PRIOR FILING DATE: 2002-02-08
;  NUMBER OF SEQ ID NOS: 308
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
;   LENGTH: 1516
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (55)..(1437)
;   OTHER INFORMATION:
US-10-316-253-39

  Query Match             18.1%;  Score 576.8;  DB 15;  Length 1516;
  Best Local Similarity   67.3%;  Pred. No. 5.3e-181;
  Matches  999;  Conservative    0;  Mismatches  257;  Indels  228;  Gaps    4;

Qy          1 CTCTGCAGCTCAGCATGGCTAGGGTACTGGAGCACCCGTTGCACTGGGGTTGTGGAGCC 60
Db         41 CTTTGCAGCTCGCCATGGCTAGGACAGTAGTAGCACTAAATATCCTGGTATTGCTGGGCC 100

Qy         61 TATGCTGGTCTCTGGCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTG 120
Db        101 TGTGCTGGTCCCTGGCTGTTGCCAACCCTCTTCCTGCTGCCCATGAGACTGTTGCTAAAG 160

Qy        121 CTGAAGGCGAGACCAAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCT 180
Db        161 GTGAAAATGGGACCAAGCCAGACTCAGATGTAATCGAACACTGCTCAGATGCCTGGAGCT 220

Qy        181 TTGATGCTACCACCCTGGATGACAATGGAACCATGCTGTTTTTAAAGGGGAGTTTGTGT 240
Db        221 TTGACGCTACCACCATGGATCACAATGGACCATGCTGTTCTTTAAAGGGGAGTTTGTGT 280
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Qy        241 GGAAGAGTCACAAATGGGACCGGGAGTTAATCTCAGAGAGATGGAAGAATTTCCCCAGCC 300
              ||| | |||||  | ||  ||||||||||||||||||||| |||||||||  |  || |
Db        281 GGAGGGGTCACTCAGGGATCCGGGAGTTAATCTCAGAGAGGTGGAAGAATCCCGTCACCT 340

Qy        301 CTGTGGATGCTGCATTCCGTCAAGGTCACAACAGTGTCTTTCTGATCAAGGGGGACAAAG 360
              | ||||||||||||||||||   ||||   |||||||||| ||||||||||  |||||||
Db        341 CAGTGGATGCTGCATTCCGT---GGTCCTGACAGTGTCTTCCTGATCAAGGAAGACAAAG 397

Qy        361 TCTGGGTATACCCTCCTGAAAAGAAGGAGAAAGGATACCCAAAGTTGCTCCAAGATGAAT 420
              ||||||| || |||||||||||||| ||||| || || ||||||||| ||||||| || |
Db        398 TCTGGGTGTATCCTCCTGAAAAGAAAGAGAACGGGTATCCAAAGTTGTTCCAAGAAGAGT 457

Qy        421 TTCCTGGAATCCCATCCCCACTGGATGCAGCTGTGGAATGTCACCGTGGAGAATGTCAAG 480
               |||||||||||||| |||||  || |||||||||||||| |||||||||||||| ||
Db        458 CTCCTGGAATCCCATACCCACCAGACGCAGCTGTGGAATGCCACCGTGGAGAATGCCAGA 517

Qy        481 CTGAAGGCGTCCTCTTCTTCCAAGGCCA-------------------------------- 508
               |||||| |||||||||||||||||  |
Db        518 GTGAAGGTGTCCTCTTCTTCCAAGGTAACCGCAAGTGGTTCTGGGACTTTGCCACAAGAA 577

Qy        509 ------------------------------------------------------------ 508

Db        578 CCCAAAAGGAACGTTCCTGGCCTGCTGTTGGGAATTGCACTGCGGCCTTGAGGTGGCTTG 637

Qy        509 ------------------------------------------------------------ 508

Db        638 AACGCTACTACTGCTTCCAGGGTAACAAGTTCCTGAGATTTAACCCCGTCACAGGAGAGG 697

Qy        509 ------------------------------------------------------------ 508

Db        698 TGCCTCCCAGATACCCTCTGGATGCCCGTGACTACTTCATATCCTGCCCTGGCAGAGGCC 757

Qy        509 ----TGGACACAGGAATGGGACTGGCCATGGGAACAGTACCCACCATGGCCCTGAGTATA 564
                  |  ||  || ||||| ||||  |||||||| || |||||       |||  | ||
Db        758 ATGGTAAACTAAGAAATGGAACTGCTCATGGGAATAGCACCCA------TCCTATGCATT 811

Qy        565 TGCGCTGTAGCCCACATCTAGTCTTGTCTGCACTGACGTCTGACAACCATGGTGCCACCT 624
               ||| |||| | || |||  | | |||||||||||  ||||||| | |  ||||||||||
Db        812 CGCGTTGTAACGCAGATCCTGGCCTGTCTGCACTGCTGTCTGACCATCGAGGTGCCACCT 871

Qy        625 ATGCCTTCAGTGGGACCCACTACTGGCGTCTGGACACCAGCCGGGATGGCTGGCATAGCT 684
              |||||||||||||  |||||||||||||||||||| ||||||| ||||| ||||||||||
Db        872 ATGCCTTCAGTGGCTCCCACTACTGGCGTCTGGACTCCAGCCGTGATGGGTGGCATAGCT 931

Qy        685 GGCCCATTGCTCATCAGTGGCCCCAGGGTCCTTCAGCAGTGGATGCTGCCTTTTCCTGGG 744
              |||||||||||||||| ||||||||||||||||||||||| |||||||||||||||||||
Db        932 GGCCCATTGCTCATCACTGGCCCCAGGGTCCTTCAGCAGTAGATGCTGCCTTTTCCTGGG 991

Qy        745 AAGAAAAACTCTATCTGGTCCAGGGCACCCAGGTATATGTCTTCCTGACAAAGGGAGGCT 804
              | || ||| |||||||| |||||||||| || ||||||||||||||||| ||||| |||
Db        992 ATGAGAAAGTCTATCTGATCCAGGGCACTCAAGTATATGTCTTCCTGACGAAGGGGGGCA 1051

Qy        805 ATACCCTAGTAAGCGGTTATCCGAAGCGGCTGGAGAAGGAAGTCGGGACCCCTCATGGGA 864
              ||| ||||||||| |||||||| |||||||||||||||||| | |||| |||||  ||||
Db       1052 ATAACCTAGTAAGTGGTTATCCAAAGCGGCTGGAGAAGGAACTTGGGAGCCCTCCCGGGA 1111

Qy        865 TTATCCTGGACTCTGTGGATGCGGCCTTTATCTGCCCTGGGTCTTCTCGGCTCCATATCA 924
              | | ||| ||  |  | ||||| ||||||  ||||||||| |||||   |||| |  |||
Db       1112 TCAGCCTTGATACCATAGATGCAGCCTTTTCCTGCCCTGGTTCTTCCAAGCTCTACGTCA 1171

Qy        925 TGGCAGGACGGCGGCTGTGGTGGCTGGACCTGAAGTCAGGAGCCCAAGCCACGTGGACAG 984
                 ||||||||||||| ||||||||||||||||||||||||||||| || || ||| |||
Db       1172 CATCAGGACGGCGGCTTTGGTGGCTGGACCTGAAGTCAGGAGCCCAGGCGACATGGGCAG 1231

Qy        985 AGCTTCCTTGGCCCCATGAGAAGGTAGACGGAGCCTTGTGTATGGAAAAGTCCCTTGGCC 1044
              ||||| | |||||||||||||| || || || ||| ||||| |||||||||||||||| |
Db       1232 AGCTTTCCTGGCCCCATGAGAAAGTTGATGGTGCCCTGTGTTTGGAAAAGTCCCTTGGTC 1291

Qy       1045 CTAACTCATGTTCCGCCAATGGTCCCGGCTTGTACCTCATCCATGGTCCCAATTTGTACT 1104
              |  ||||||| ||  |||||||||||  ||||| | | |||||||| |||||||| ||||
Db       1292 CCTACTCATGCTCTTCCAATGGTCCCAACTTGTTCTTTATCCATGGGCCCAATTTATACT 1351

Qy       1105 GCTACAGTGATGTGGAGAAACTGAATGCAGCCAAGGCCCTTCCGCAACCCCAGAATGTGA 1164
              |||| ||   | | || ||||||||||||||||||   || || || |||||||| ||||
Db       1352 GCTATAGCAGTATAGACAAACTGAATGCAGCCAAGAGTCTGCCTCAGCCCCAGAAAGTGA 1411

Qy       1165 CCAGTCTCCTGGGCTGCACTCACTGAGGGGCC---TTCTGACATGAGTCTGGCCTGGCCC 1221
               |||  |||| ||||||| ||| | |   |||    |  ||  |    | | ||   ||
Db       1412 ACAGCATCCTTGGCTGCAGTCAATAAAAAGCCCTGATGGGAATTAGCCCAGCCCACCCCA 1471

Qy       1222 CACCTCCTAGTTCCTCATAATAAAGACAGATTGCTTCTTCGCTT 1265
              |  ||||   | | |  |||||||  ||||| | |||||| | |
Db       1472 CCTCTCCATTTCCATTCTAATAAAACCAGATGGTTTCTTCACAT 1515


RESULT 8
US-09-918-995-30828
; Sequence 30828, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 30828
;   LENGTH: 488
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(488)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-30828

  Query Match             13.4%;  Score 427;  DB 10;  Length 488;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-131;
  Matches  427;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GCAGCTCAGCATGGCTAGGGTACTGGGAGCACCCGTTGCACTGGGGTTGTGGAGCCTATG 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCAGCTCAGCATGGCTAGGGTACTGGGAGCACCCGTTGCACTGGGGTTGTGGAGCCTATG 120

Qy         65 CTGGTCTCTGGCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTGCTGA 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGGTCTCTGGCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTGCTGA 180

Qy        125 AGGCGAGACCAAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCTTTGA 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGGCGAGACCAAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCTTTGA 240

Qy        185 TGCTACCACCCTGGATGACAATGGAACCATGCTGTTTTTTAAAGGGGAGTTTGTGTGGAA 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCTACCACCCTGGATGACAATGGAACCATGCTGTTTTTTAAAGGGGAGTTTGTGTGGAA 300

Qy        245 GAGTCACAAATGGGACCGGGAGTTAATCTCAGAGAGATGGAAGAATTTCCCCAGCCCTGT 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGTCACAAATGGGACCGGGAGTTAATCTCAGAGAGATGGAAGAATTTCCCCAGCCCTGT 360

Qy        305 GGATGCTGCATTCCGTCAAGGTCACAACAGTGTCTTTCTGATCAAGGGGGACAAAGTCTG 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGATGCTGCATTCCGTCAAGGTCACAACAGTGTCTTTCTGATCAAGGGGGACAAAGTCTG 420

Qy        365 GGTATACCCTCCTGAAAAGAAGGAGAAAGGATACCCAAAGTTGCTCCAAGATGAATTTCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGTATACCCTCCTGAAAAGAAGGAGAAAGGATACCCAAAGTTGCTCCAAGATGAATTTCC 480

Qy        425 TGGAATC 431
              |||||||
Db        481 TGGAATC 487
```

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RESULT 9
US-09-918-995-8595
; Sequence 8595, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8595
;   LENGTH: 422
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-918-995-8595

  Query Match             13.2%;  Score 421;  DB 10;  Length 422;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-129;
  Matches  421;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TCTGCAGCTCAGCATGGCTAGGGTACTGGAGCACCCGTTGCACTGGGGTTGTGGAGCCT 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCTGCAGCTCAGCATGGCTAGGGTACTGGAGCACCCGTTGCACTGGGGTTGTGGAGCCT 60

Qy         62 ATGCTGGTCTCTGGCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTGC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGCTGGTCTCTGGCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTGC 120

Qy        122 TGAAGGCGAGACCAAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCTT 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGAAGGCGAGACCAAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCTT 180

Qy        182 TGATGCTACCACCCTGGATGACAATGGAACCATGCTGTTTTTTAAAGGGGAGTTTGTGTG 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGATGCTACCACCCTGGATGACAATGGAACCATGCTGTTTTTTAAAGGGGAGTTTGTGTG 240

Qy        242 GAAGAGTCACAAATGGGACCGGGAGTTAATCTCAGAGAGATGGAAGAATTTCCCCAGCCC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAGAGTCACAAATGGGACCGGGAGTTAATCTCAGAGAGATGGAAGAATTTCCCCAGCCC 300

Qy        302 TGTGGATGCTGCATTCCGTCAAGGTCACAACAGTGTCTTTCTGATCAAGGGGGACAAAGT 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTGGATGCTGCATTCCGTCAAGGTCACAACAGTGTCTTTCTGATCAAGGGGGACAAAGT 360

Qy        362 CTGGGTATACCCTCCTGAAAAGAAGGAGAAAGGATACCCAAAGTTGCTCCAAGATGAATT 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGGGTATACCCTCCTGAAAAGAAGGAGAAAGGATACCCAAAGTTGCTCCAAGATGAATT 420

Qy        422 T 422
              |
Db        421 T 421

RESULT 10
US-09-918-995-31395
; Sequence 31395, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31395
;   LENGTH: 492
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(492)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31395

  Query Match             13.1%;  Score 417;  DB 10;  Length 492;
  Best Local Similarity   97.1%;  Pred. No. 7.1e-128;
  Matches  434;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          5 GCAGCTCAGCATGGCTAGGGTACTGGAGCACCCGTTGCACTGGGGTTGTGGAGCCTATG 64
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db         46 GCAGCTCAGCATGGCTAGGGTACTGGAGCACCCGATGCACTGGGGTTGTGGAGCCTATG 105

Qy         65 CTGGTCTCTGGCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTGCTGA 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 CTGGTCTCTGGCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTGCTGA 165

Qy        125 AGGCGAGACCAAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCTTTGA 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 AGGCGAGACCAAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCTTTGA 225

Qy        185 TGCTACCACCCTGGATGACAATGGAACCATGCTGTTTTTTAAAGGGGAGTTTGTGTGGAA 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 TGCTACCACCCTGGATGACAATGGAACCATGCTGTTTTTTAAAGGGGAGTTTGTGTGGAA 285

Qy        245 GAGTCACAAATGGGACCGGGAGTTAATCTCAGAGAGATGGAAGAATTTCCCCAGCCCTGT 304
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        286 GAGTCACAAATGGGACCGGGAGTTAATCTCACAGAGATGGAAGAATTTCCCCAGCCCTGT 345

Qy        305 GGATGCTGCATTCCGTCAAGGTCACAACAGTGTCTTTCTGATCAAGGGGGACAAAGTCTG 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        346 GGATGCTGCATTCCGTCAAGGTCACAACAGTGTCTTTCTGATCAAGGGGGACACAGTCTG 405

Qy        365 GGTATACCCTCCTGAAAAGAAGGAGAAAGGATACCCAAAGTTGCTCCAAGATGAATTTCC 424
               ||||||||||||||  ||||||||| ||||||||||||  ||||||||||||||||  |
Db        406 AGTATACCCTCCTGANNAGAAGGAGACAGGATACCCAAAAGTGCTCCAAGATGAATTCAC 465

Qy        425 TGGAATCCCATCCCCACTGGATGCAGC 451
              ||| ||||||| |||||||||||||||
Db        466 TGG-ATCCCATACCCACTGGATGCAGC 491

RESULT 11
US-09-918-995-30754
; Sequence 30754, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 30754
;   LENGTH: 488
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(488)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-30754
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  Query Match             11.7%;  Score 374.2;  DB 10;  Length 488;
  Best Local Similarity   99.2%;  Pred. No. 1.5e-113;
  Matches  376;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        503 AGGCCATGGACACAGGAATGGGACTGGCCATGGGAACAGTACCCACCATGGCCCTGAGTA 562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 AGGCCATGGACACAGGAATGGGACTGGCCATGGGAACAGTACCCACCATGGCCCTGAGTA 169

Qy        563 TATGCGCTGTAGCCCACATCTAGTCTTGTCTGCACTGACGTCTGACAACCATGGTGCCAC 622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 TATGCGCTGTAGCCCACATCTAGTCTTGTCTGCACTGACGTCTGACAACCATGGTGCCAC 229

Qy        623 CTATGCCTTCAGTGGACCCACTACTGGCGTCTGGACACCAGCCGGGATGGCTGGCATAG 682
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        230 CTATGCCTTCAGTGGACCCACTACTGGCGTATGGACACCAGCCGGGATGGCTGGCATAG 289

Qy        683 CTGGCCCATTGCTCATCAGTGGCCCCAGGGTCCTTCAGCAGTGGATGCTGCCTTTTCCTG 742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 CTGGCCCATTGCTCATCAGTGGCCCCAGGGTCCTTCAGCAGTGGATGCTGCCTTTTCCTG 349

Qy        743 GGAAGAAAAACTCTATCTGGTCCAGGGCACCCAGGTATATGTCTTCCTGACAAAGGGAGG 802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 GGAAGAAAAACTCTATCTGGTCCAGGGCACCCAGGTATATGTCTTCCTGACAAAGGGAGG 409

Qy        803 CTATACCCTAGTAAGCGGTTATCCGAAGCGGCTGGAGAAGGAAGTCGGACCCCTCATGG 862
              |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db        410 CTATACCCTAGTAAGCGGTTATCCGAAGCGGCTGGAGAAGGAAGACGGACCCCTCATGG 469

Qy        863 GATTATCCTGGACTCTGTG 881
              |||||| ||||||||||||
Db        470 GATTATGCTGGACTCTGTG 488


RESULT 12
US-09-918-995-32820
; Sequence 32820, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32820
;   LENGTH: 491
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(491)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32820

  Query Match             10.8%;  Score 345.4;  DB 10;  Length 491;
  Best Local Similarity   99.7%;  Pred. No. 6.3e-104;
  Matches  346;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        503 AGGCCATGGACACAGGAATGGGACTGGCCATGGGAACAGTACCCACCATGGCCCTGAGTA 562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AGGCCATGGACACAGGAATGGGACTGGCCATGGGAACAGTACCCACCATGGCCCTGAGTA 204

Qy        563 TATGCGCTGTAGCCCACATCTAGTCTTGTCTGCACTGACGTCTGACAACCATGGTGCCAC 622
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        205 TATGCGCTGTAGCCCACATCTAGTCTTGTCCGCACTGACGTCTGACAACCATGGTGCCAC 264

Qy        623 CTATGCCTTCAGTGGACCCACTACTGGCGTCTGGACACCAGCCGGGATGGCTGGCATAG 682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 CTATGCCTTCAGTGGACCCACTACTGGCGTCTGGACACCAGCCGGGATGGCTGGCATAG 324

Qy        683 CTGGCCCATTGCTCATCAGTGGCCCCAGGGTCCTTCAGCAGTGGATGCTGCCTTTTCCTG 742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 CTGGCCCATTGCTCATCAGTGGCCCCAGGGTCCTTCAGCAGTGGATGCTGCCTTTTCCTG 384

Qy        743 GGAAGAAAAACTCTATCTGGTCCAGGGCACCCAGGTATATGTCTTCCTGACAAAGGGAGG 802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GGAAGAAAAACTCTATCTGGTCCAGGGCACCCAGGTATATGTCTTCCTGACAAAGGGAGG 444

Qy        803 CTATACCCTAGTAAGCGGTTATCCGAAGCGGCTGGAGAAGGAAGTCG 849
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        445 CTATACCCTAGTAAGCGGTTATCCGAAGCGGCTGGAGAAGGAAGTCG 491


RESULT 13
US-09-880-107-3166/c
; Sequence 3166, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
;  APPLICANT: Horne, Darci T.
;  APPLICANT:  Vockley, Joseph G.
;  APPLICANT:  Scherf, Uwe
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;  FILE REFERENCE: 44921-5028-WO
;  CURRENT APPLICATION NUMBER: US/09/880,107
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/211,379
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: US 60/237,054
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 3950
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3166
;   LENGTH: 504
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20020142981A1 T61801
;   NAME/KEY: unsure
;   LOCATION: (1)..(504)
;   OTHER INFORMATION: n = a or c or g or t
US-09-880-107-3166

  Query Match              9.8%;  Score 313.4;  DB 9;  Length 504;
  Best Local Similarity   91.4%;  Pred. No. 3.2e-93;
  Matches  468;  Conservative    0;  Mismatches   29;  Indels   15;  Gaps   13;

Qy        839 GAAGGAAGTCGGACCCCTCATGGGATTATCCTGGACTCTGTGGATGCGGCCTTTATCTG 898
              |||    |     |||||| |||||| |||| ||| ||||||||| ||||||||||||||||
Db        498 GAAAAGAAGNTGGACCCNTCATGGAATTANCCT-GACTCTGTGAATGCGGCCTTTATCTG 440

Qy        899 CCCTGGGTCTTCTCGGCTCCATATCATGGCAGGACGGCGGCTGTGGTGGCTGGACCTGAA 958
              |||| |||||||||||||| ||||||||| |||||||| |||||||||||||||||||||
Db        439 CCCT-GGTCTTCTCGGCTCNATATCATGGNAGGACGGCTGCTGTGGTGGCTGGACCTGAA 381

Qy        959 GTCAGGAGCCCAAGCCACGTGGACAGAGCTTCCTTGG-CCCCATGAGAAGGTAGACGGAG 1017
              |||||||  |||||||||||||| ||||||||||||| ||||||||||||||||||||||
Db        380 GTCAGGA-NCCAAGCCACGTGGANAGAGCTTCCTTGGNCCCCATGAGAAGGTAGACGGAG 322

Qy       1018 CCTTGTGTATGGAAAAGTCCCTTGGCCCTAACTCATGTTCCGCCAATGGTCCCGGCTTGT 1077
              ||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||||
Db        321 CCTTGTGTATGGAAAAGNC-CTTGGCCCTAACTCATGTTCCGCCAATGGTCCCGGCTTGT 263

Qy       1078 ACCTCATCCATGGTCCCAATTTGTACTGCTACAGTGATGTGGAGAAACTGAATGCAGCCA 1137
              ||||||||||||| ||||||||||||||||| ||||||||||||||||||||||||  ||
Db        262 ACCTCATCCATGG-CCCAATTTGTACTGCTANAGTGATGTGGAGAAACTGAATGCA-NCA 205

Qy       1138 AGGCCCTTCCGCAACCCCAGAATGTGACCAGTCTCCTGGGCTGCACTCACTGAGGGGCCT 1197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        204 AGGCCCTTCCGCAACCCCAGAATGTGACCAGTCTCCTGGGCTGCACTCACTGA-GGGCCT 146

Qy       1198 TCTGACATGAGTCTGGCCTGGCCCCACCTCCTAGTTCCTCATAATAAAGACAGATTGCTT 1257
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               |||||||||||||||  |  | |||||||||||| |||||||||||||||||||||||||
Db         145 TCTGACATGAGTCTG--CCTGGCCCACCTCCTAG-TCCTCATAATAAAGACAGATTGCTT 89

Qy        1258 CTTCGCTTCTCACTGAGGGGCCTTCTGACATGAGTCTGGCCTGGCCCCACCTCCCCAGTT 1317
               ||| |||||||||||| ||| |||||||||||||||||  |  | |||||||||||||||
Db          88 CTT-GCTTCTCACTGA-GGGNCTTCTGACATGAGTCTG--CCTGNCCCACCTCCCCAGTT 33

Qy        1318 TCTCATAATAAAGACAGATTGCTTCTTCACTT 1349
               ||||||||||||||||||||||   |||||||
Db          32 TCTCATAATAAAGACAGATTGCAANTTCACTT 1


RESULT 14
US-09-960-352-10323
; Sequence 10323, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 10323
;   LENGTH: 420
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 44-LIB34-041-Q1-E1-C8
US-09-960-352-10323

  Query Match             9.4%;  Score 298.4;  DB 9;  Length 420;
  Best Local Similarity   81.9%;  Pred. No. 3e-88;
  Matches  344;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy         663 AGCCGGGATGGCTGGCATAGCTGGCCCATTGCTCATCAGTGGCCCCAGGGTCCTTCAGCA 722
               |||||||| || ||||| ||||||| |||||  |||| ||||||||| ||||| ||| ||
Db           1 AGCCGGGACGGGTGGCACAGCTGGCTCATTGAGCATCTGTGGCCCCAAGGTCCCTCAACA 60

Qy         723 GTGGATGCTGCCTTTTCCTGGGAAGAAAAACTCTATCTGGTCCAGGGCACCCAGGTATAT 782
               |||||||||||||||  ||||||  |||| ||||| ||  ||||||| ||||||||||||
Db          61 GTGGATGCTGCCTTTCTCTGGGATAAAAAGCTCTACCTCATCCAGGGTACCCAGGTATAT 120

Qy         783 GTCTTCCTGACAAAGGGAGGCTATACCCTAGTAAGCGGTTATCCGAAGCGGCTGGAGAAG 842
                |||||||||||| || |||||| || || ||||  | |||||| |||| ||||||||||
Db         121 ATCTTCCTGACAAGGGCAGGCTACACTCTCGTAAAAGATTATCCAAAGCAGCTGGAGAAG 180

Qy         843 GAAGTCGGGACCCCTCATGGGATTATCCTGGACTCTGTGGATGCGGCCTTTATCTGCCCT 902
               ||| | |||| |||| ||||| |   |||  | ||||||||||| ||||||| ||| |||
Db         181 GAATTTGGGAGCCCTGATGGGGTCTGCCTTCATTCTGTGGATGCAGCCTTTACCTGTCCT 240

Qy         903 GGGTCTTCTCGGCTCCATATCATGGCAGGACGGCGGCTGTGGTGGCTGGACCTGAAGTCA 962
               || ||||||| |||| | ||||||||| | | |  ||||||| ||||||||||||| | |
Db         241 GGATCTTCTCAGCTCTACATCATGGCACGCCAGAAGCTGTGGAGGCTGGACCTGAACTTA 300

Qy         963 GGAGCCCAAGCCACGTGGACAGAGCTTCCTTGGCCCCATGAGAAGGTAGACGGAGCCTTG 1022
               ||||| |||||||||||||||||||||||||||| ||||  ||| || || || ||| ||
Db         301 GGAGCTCAAGCCACGTGGACAGAGCTTCCTTGGCTCCATACGAAAGTCGATGGGGCCCTG 360

Qy        1023 TGTATGGAAAAGTCCCTTGGCCCTAACTCATGTTCCGCCAATGGTCCCGGCTTGTACCTC 1082
               ||||  || ||||| || |||||  |||| ||||| ||||||||||  ||||||||||||
Db         361 TGTACAGAGAAGTCTCTGGGCCCCCACTCGTGTTCTGCCAATGGTCGGGGCTTGTACCTC 420


RESULT 15
US-09-960-352-7040
; Sequence 7040, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 7040
;   LENGTH: 408
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 30-LIB34-026-Q1-E1-H5
US-09-960-352-7040

  Query Match             8.8%;  Score 280;  DB 9;  Length 408;
  Best Local Similarity   80.4%;  Pred. No. 4.2e-82;
  Matches  328;  Conservative    0;  Mismatches   80;  Indels    0;  Gaps    0;

Qy         767 GGGCACCCAGGTATATGTCTTCCTGACAAAGGGAGGCTATACCCTAGTAAGCGGTTATCC 826
               ||| |||||||||||| |||||||||||| || |||||| || || ||||  | ||||||
Db           1 GGGTACCCAGGTATATATCTTCCTGACAAGGGCAGGCTACACTCTCGTAAAAGATTATCC 60

Qy         827 GAAGCGGCTGGAGAAGGAAGTCGGGACCCCTCATGGGATTATCCTGGACTCTGTGGATGC 886
                |||| ||||||||||||| | |||| |||| ||||| |   |||  | |||||||||||
Db          61 AAAGCAGCTGGAGAAGGAATTTGGGAGCCCTGATGGGGTCTGCCTTCATTCTGTGGATGC 120

Qy         887 GGCCTTTATCTGCCCTGGGTCTTCTCGGCTCCATATCATGGCAGGACGGCGGCTGTGGTG 946
                ||||||| ||| ||||| ||||||| |||| | ||||||||||| | |  ||||||| |
Db         121 AGCCTTTACCTGTCCTGGATCTTCTCAGCTCTACATCATGGCAGGCCAGAAGCTGTGGAG 180

Qy         947 GCTGGACCTGAAGTCAGGAGCCCAAGCCACGTGGACAGAGCTTCCTTGGCCCCATGAGAA 1006
               |||||||||||| | |||||| |||||||||||||||||||||||||||| ||||  |||
Db         181 GCTGGACCTGAACTTAGGAGCTCAAGCCACGTGGACAGAGCTTCCTTGGCTCCATACGAA 240

Qy        1007 GGTAGACGGAGCCTTGTGTATGGAAAAGTCCCTTGGCCCTAACTCATGTTCCGCCAATGG 1066
                || || || ||| ||||||  || ||||| || |||||  |||| ||||| ||||||||
Db         241 AGTCGATGGGGCCCTGTGTACAGAGAAGTCTCTGGGCCCCCACTCGTGTTCTGCCAATGG 300

Qy        1067 TCCCGGCTTGTACCTCATCCATGGTCCCAATTTGTACTGCTACAGTGATGTGGAGAAACT 1126
               ||  |||||||||||| |||| || |||||| ||||||||||||  ||||||||| || |
Db         301 TCTGGGCTTGTACCTCGTCCAAGGCCCCAATCTGTACTGCTACAAAGATGTGGAGGAATT 360

Qy        1127 GAATGCAGCCAAGGCCCTTCCGCAACCCCAGAATGTGACCAGTCTCCT 1174
               ||      |||||| |||||| ||  ||||||   ||| ||| |||||
Db         361 GAGCAAGACCAAGGACCTTCCCCAGGCCCAGAGGATGAACAGCCTCCT 408


Search completed: June  8, 2004, 06:00:01
Job time : 1300 secs
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                GenCore version 5.1.6
         Copyright (c) 1993 - 2004  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         June  8, 2004, 01:43:13 ; Search time 197 Seconds
                                          (without alignments)
                                          8974.993 Million cell updates/sec

Title:          US-09-900-448-1
Perfect score:  3186
Sequence:       1 ctctgcagctcagcatggct..........accttttgctgtgttctca 3186

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters:      1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_NA:*
                 1:  /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2:  /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3:  /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                 4:  /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                 5:  /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6:  /cgn2_6/ptodata/2/ina/backfiles1.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                 SUMMARIES
                %
Result          Query
  No.    Score  Match Length DB ID                    Description
-----------------------------------------------------------------------
     1      88    2.8   3001  4 US-09-539-333D-177    Sequence 177, App
c    2      86    2.7  87350  3 US-08-781-891-79      Sequence 79, Appl
c    3      86    2.7  87350  4 US-09-618-166-79      Sequence 79, Appl
c    4      86    2.7  87543  4 US-09-791-211-3       Sequence 3, Appli
c    5    83.2    2.6    503  4 US-09-621-976-3523    Sequence 3523, Ap
     6    82.6    2.6  48763  4 US-09-916-204-3       Sequence 3, Appli
     7    82.6    2.6 174493  4 US-09-804-471A-3      Sequence 3, Appli
     8    82.6    2.6 174493  4 US-10-238-709-3       Sequence 3, Appli
c    9    82.2    2.6 161652  4 US-09-497-855A-40     Sequence 40, Appl
    10    80.8    2.5  63588  4 US-09-873-404-3       Sequence 3, Appli
    11    80.4    2.5  50000  4 US-09-146-053-4       Sequence 4, Appli
    12    79.2    2.5 193303  4 US-09-497-855A-37     Sequence 37, Appl
    13    79.2    2.5 193303  4 US-09-497-855A-44     Sequence 44, Appl
    14      79    2.5   1001  4 US-09-671-317-212     Sequence 212, App
    15      79    2.5   1001  4 US-09-671-317-458     Sequence 458, App
c   16    78.4    2.5   8353  3 US-08-611-587-1       Sequence 1, Appli
c   17    77.6    2.4  72928  3 US-09-009-913-1       Sequence 1, Appli
c   18    69.2    2.2   1282  4 US-09-205-258-197     Sequence 197, App
c   19      69    2.2  50000  4 US-09-146-053-3       Sequence 3, Appli
c   20    68.4    2.1 197496  4 US-09-877-177A-10     Sequence 10, Appl
    21    68.2    2.1    309  4 US-09-222-575-145     Sequence 145, App
    22    68.2    2.1    309  4 US-09-389-681-145     Sequence 145, App
    23    68.2    2.1    309  4 US-09-620-405B-145    Sequence 145, App
    24    68.2    2.1    309  4 US-09-339-338-145     Sequence 145, App
    25    68.2    2.1    309  4 US-09-433-826B-145    Sequence 145, App
    26    68.2    2.1    309  4 US-09-604-287A-145    Sequence 145, App
    27    68.2    2.1    309  4 US-09-285-480-145     Sequence 145, App
    28    68.2    2.1    309  4 US-09-834-759-145     Sequence 145, App
c   29    67.8    2.1  50000  4 US-09-146-053-4       Sequence 4, Appli
    30    67.6    2.1   2060  4 US-09-640-173-183     Sequence 183, App
    31    67.6    2.1   2060  4 US-09-713-550-183     Sequence 183, App
    32    67.6    2.1   3000  4 US-09-640-173-185     Sequence 185, App
    33    67.6    2.1   3000  4 US-09-713-550-185     Sequence 185, App
    34    66.8    2.1  41684  4 US-09-536-059-1       Sequence 1, Appli
    35    66.6    2.1   1001  4 US-09-641-638-459     Sequence 459, App
c   36    66.6    2.1 392000  4 US-10-027-983-11      Sequence 11, Appl
c   37    65.8    2.1   7218  1 US-08-232-463-14      Sequence 14, Appl
    38    63.4    2.0 786431  4 US-09-751-389-3       Sequence 3, Appli
c   39    63.2    2.0 246240  2 US-08-724-394A-20     Sequence 20, Appl
c   40    63.2    2.0 246240  2 US-08-724-394A-21     Sequence 21, Appl
c   41    63.2    2.0 246240  2 US-08-724-394A-22     Sequence 22, Appl
c   42      63    2.0   3001  4 US-09-539-333D-192    Sequence 192, App
c   43    62.8    2.0  44453  4 US-09-146-053-5       Sequence 5, Appli
c   44      62    1.9 319608  4 US-09-539-333D-1      Sequence 1, Appli
c   45      62    1.9 319608  4 US-09-679-409-1       Sequence 1, Appli

                                 ALIGNMENTS

RESULT 1
US-09-539-333D-177
; Sequence 177, Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Essioux, Laurent
;  TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
;  FILE REFERENCE: GENSET.047AUS
;  CURRENT APPLICATION NUMBER: US/09/539,333D
;  CURRENT FILING DATE:  2000-03-30
;  PRIOR APPLICATION NUMBER: US 60/126,903
;  PRIOR FILING DATE: 1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/131,971
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/132,065
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: US 60/143,928
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: US 60/145,915
;  PRIOR FILING DATE: 1999-07-27
;  PRIOR APPLICATION NUMBER: US 60/146,453
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/146,452
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 60/162,288
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: US 09/416,384
;  PRIOR FILING DATE: 1999-10-12
;  NUMBER OF SEQ ID NOS: 231
;  SOFTWARE: Patent.pm
; SEQ ID NO 177
;   LENGTH: 3001
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 1501
;   OTHER INFORMATION: 99-15668-139 : polymorphic base C or T
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: 1482..1500
;   OTHER INFORMATION: 99-15668-139.mis1
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: 1502..1521
;   OTHER INFORMATION: 99-15668-139.mis2,  complement
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1363..1380
;   OTHER INFORMATION: upstream amplification primer
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1801..1821
;   OTHER INFORMATION: downstream amplification primer, complement
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: 1489..1513
;   OTHER INFORMATION: 99-15668-139  probe
US-09-539-333D-177

  Query Match             2.8%;  Score 88;  DB 4;  Length 3001;
  Best Local Similarity   71.7%;  Pred. No. 8.9e-18;
  Matches  129;  Conservative    0;  Mismatches   50;  Indels    1;  Gaps    1;

Qy       3008 GTTTCAGTCAGTTTAGGCTGCTATAAGAGAATATCTTAGAGTGGGTAATCTATCAGCAAT 3067
              |||  |||||||||  |||||| ||| |||||| |  ||| ||||| ||  || |  ||
Db       2055 GTTCTAGTCAGTTTTTGCTGCTGTAACAGAATACCACAGACTGGGTCATTAATAAAGAAG 2114

Qy       3068 AGGAATTTATTGTTCACAATTCTGGAGGCTGGAAAATCCAAGATCAAGGCTCCAGCAGGT 3127
              | ||||| |||  ||| | || |||||||| |||| ||| |||| ||||| ||||||  |
Db       2115 AAGAATTCATTTCTCATAGTTGTGGAGGCTAGAAAGTCCGAGATGAAGGCGCCAGCAAAT 2174

Qy       3128 TCAGTGTCTGCTGAGTGCT-TGTTCTGCTTCGAAGATGGCACCTTTTTGCTGTGTTCTCA 3186
              |  |||| || |  | | |  | |||||||| |||||| | | ||  |||||  || |||
Db       2175 TTGGTGTGTGGTAGGGGTTGCGCTCTGCTTCCAAGATGACGCTTTGATGCTGCATTTTCA 2234

RESULT 2
US-08-781-891-79/c
; Sequence 79, Application US/08781891
; Patent No. 6090620
;  GENERAL INFORMATION:
;    APPLICANT:  Fu, Ying-Hui
;    APPLICANT:  Yu, Chang-En
;    APPLICANT:  Oshima, Junko
;    APPLICANT:  Mulligan, John T.
;    APPLICANT:  Schellenberg, Gerald D.
;    TITLE OF INVENTION:  GENE AND GENE PRODUCTS RELATED TO
;    TITLE OF INVENTION:  WERNER'S SYNDROME
;    NUMBER OF SEQUENCES:  209
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/781,891
;      FILING DATE:  27-DEC-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6090620tenburg Ph.D., Carol
;      REGISTRATION NUMBER:  39,317
;      REFERENCE/DOCKET NUMBER:  240052.419
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  79:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  87350 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-781-891-79

  Query Match             2.7%;  Score 86;  DB 3;  Length 87350;
  Best Local Similarity   73.3%;  Pred. No. 4.8e-16;
  Matches  151;  Conservative    0;  Mismatches   50;  Indels    5;  Gaps    3;

Qy       2983 TCCAGGGAACTCCCAGAAATGGTTTGTTTCAGTCAGTTTAGGCTGCT---ATAAGAGAAT 3039
              | |  | |  | |||||| || ||||| | |||| ||||  |||| |   |||| | |||
Db      68776 TACTAGTATGTGCCAGAACTGATTTGTCTTAGTCTGTTTTTGCTGTTTTCATAACAAAAT 68717

Qy       3040 ATCTTAGAGTGGGTAATCTATCAGCAATAGGAATTTATTGTTCACAATTCTGGAGGCTGG 3099
                |  ||| |||| ||| ||  | ||| || | ||||||  ||| | |||||||||||||
Db      68716 GCCACAGACTGGGCAATTTACAAACAACAGTAGTTTATTTCTCATAGTTCTGGAGGCTGG 68657

Qy       3100 AAAATCCAAGATCAAGGCTCCAGCAGGTTCAGTGTCTGCTGAGTGCTTGT-TCTGCTTCG 3158
               |  |||||||||||||| |||| |||||||||||||| |||| |||  | ||||||||
Db      68656 -AGGTCCAAGATCAAGGCGCCAGTAGGTTCAGTGTCTGGTGAGGGCTGCTCTCTGCTTCC 68598

Qy       3159 AAGATGGCACCTTTTTGCTGTGTTCT 3184
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Db      68597 AAAATGGAGGCTTGTCGCTGTGTCCT 68572

RESULT 3
US-09-618-166-79/c
; Sequence 79, Application US/09618166
; Patent No. 6583112
;  GENERAL INFORMATION:
;       APPLICANT: Fu, Ying-Hui
;                  Yu, Chang-En
;                  Oshima, Junko
;                  Mulligan, John T.
;                  Schellenberg, Gerald D.
;       TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
;                          WERNER'S SYNDROME
;       NUMBER OF SEQUENCES: 209
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Seed Intellectual Property Law Group
;            STREET: 701 Fifth Avenue, Suite 6300
;            CITY: Seattle
;            STATE: Washington
;            COUNTRY: USA
;            ZIP: 98104-7092
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/618,166
;            FILING DATE: 17-Jul-2000
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McMasters, David D.
;            REGISTRATION NUMBER: 33,963
;            REFERENCE/DOCKET NUMBER: 240052.419C1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (206) 622-4900
;            TELEFAX: (206) 682-6031
;  INFORMATION FOR SEQ ID NO: 79:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 87350 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-618-166-79

  Query Match             2.7%;  Score 86;  DB 4;  Length 87350;
  Best Local Similarity   73.3%;  Pred. No. 4.8e-16;
  Matches  151;  Conservative    0;  Mismatches   50;  Indels    5;  Gaps    3;
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Qy       2983 TCCAGGGAACTCCCAGAAATGGTTTGTTTCAGTCAGTTTAGGCTGCT---ATAAGAGAAT 3039
              | |  | |  | |||||| || ||||| | |||| ||||  |||| |   |||| | |||
Db      68776 TACTAGTATGTGCCAGAACTGATTTGTCTTAGTCTGTTTTTGCTGTTTTCATAACAAAAT 68717

Qy       3040 ATCTTAGAGTGGGTAATCTATCAGCAATAGGAATTTATTGTTCACAATTCTGGAGGCTGG 3099
                |  ||| |||| ||| ||  | ||| || | ||||||  ||| | |||||||||||||
Db      68716 GCCACAGACTGGGCAATTTACAAACAACAGTAGTTTATTTCTCATAGTTCTGGAGGCTGG 68657

Qy       3100 AAAATCCAAGATCAAGGCTCCAGCAGGTTCAGTGTCTGCTGAGTGCTTGT-TCTGCTTCG 3158
               |  |||||||||||||| |||| |||||||||||||| |||| |||  | ||||||||
Db      68656 -AGGTCCAAGATCAAGGCGCCAGTAGGTTCAGTGTCTGGTGAGGGCTGCTCTCTGCTTCC 68598

Qy       3159 AAGATGGCACCTTTTTGCTGTGTTCT 3184
              || ||||   ||| | ||||||| ||
Db      68597 AAAATGGAGGCTTGTCGCTGTGTCCT 68572

RESULT 4
US-09-791-211-3/c
; Sequence 3, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
;  APPLICANT:  Donna T. Ward
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION:  ANTISENSE MODULATION OF WRN EXPRESSION
;  FILE REFERENCE:  RTS-0205
;  CURRENT APPLICATION NUMBER: US/09/791,211
;  CURRENT FILING DATE:  2001-02-23
;  NUMBER OF SEQ ID NOS:  90
; SEQ ID NO 3
;   LENGTH: 87543
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 7421
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 7427
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 11609
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 12605
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 12742
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29370
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29422
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29979
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29980
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29981
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 30136
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 30140
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 31205
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 31206
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 31592
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 33095
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 33160
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 34066
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 34072
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 36816
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 39020
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 42164
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 42459
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 46808
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 46823
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 46826
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 47291
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 52786
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 52787
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 53384
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 54684
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 59215
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 59235
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 59242
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 63290
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 66614
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 68660
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 68697
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 68718
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 68733
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 68739
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 69785
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 79134
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 79198
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 86336
;   OTHER INFORMATION: unknown
;   OTHER INFORMATION:
US-09-791-211-3

  Query Match             2.7%;  Score 86;  DB 4;  Length 87543;
  Best Local Similarity   73.3%;  Pred. No. 4.8e-16;
  Matches  151;  Conservative    0;  Mismatches   50;  Indels    5;  Gaps    3;

Qy       2983 TCCAGGGAACTCCCAGAAATGGTTTGTTTCAGTCAGTTTAGGCTGCT---ATAAGAGAAT 3039
              | |  | |  | |||||| || ||||| | |||| ||||  |||| |   |||| | |||
Db      68969 TACTAGTATGTGCCAGAACTGATTTGTCTTAGTCTGTTTTTGCTGTTTTCATAACAAAAT 68910

Qy       3040 ATCTTAGAGTGGGTAATCTATCAGCAATAGGAATTTATTGTTCACAATTCTGGAGGCTGG 3099
                |  ||| |||| ||| ||  | ||| || | ||||||  ||| | |||||||||||||
Db      68909 GCCACAGACTGGGCAATTTACAAACAACAGTAGTTTATTTCTCATAGTTCTGGAGGCTGG 68850

Qy       3100 AAAATCCAAGATCAAGGCTCCAGCAGGTTCAGTGTCTGCTGAGTGCTTGT-TCTGCTTCG 3158
               |  |||||||||||||| |||| |||||||||||||| |||| |||  | ||||||||
Db      68849 -AGGTCCAAGATCAAGGCGCCAGTAGGTTCAGTGTCTGGTGAGGGCTGCTCTCTGCTTCC 68791

Qy       3159 AAGATGGCACCTTTTTGCTGTGTTCT 3184
              || ||||   ||| | ||||||| ||
Db      68790 AAAATGGAGGCTTGTCGCTGTGTCCT 68765


RESULT 5
US-09-621-976-3523/c
; Sequence 3523, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 3523
;   LENGTH: 503
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 134..382
US-09-621-976-3523

  Query Match             2.6%;  Score 83.2;  DB 4;  Length 503;
  Best Local Similarity   75.7%;  Pred. No. 9.2e-17;
  Matches  103;  Conservative    0;  Mismatches   33;  Indels    0;  Gaps    0;
```

```
Qy       3019 TTTAGGCTGCTATAAGAGAATATCTTAGAGTGGGTAATCTATCAGCAATAGGAATTTATT 3078
              |||| || ||||||| |||||| |||||  || ||||| ||| |  ||||  ||| |||
Db        386 TTTATGCAGCTATAACAGAATACCTTAGCATGAGTAATATATAAATAATAAAAATGTATG 327

Qy       3079 GTTCACAATTCTGGAGGCTGGAAAATCCAAGATCAAGGCTCCAGCAGGTTCAGTGTCTGC 3138
                | ||| | ||| ||| || |||||||||||||| ||| |  |||||||  ||||||||
Db        326 TCTTACAGTCCTGCAGGTTGAAAAATCCAAGATCATGGCACTGGCAGGTTTTGTGTCTGC 267

Qy       3139 TGAGTGCTTGTTCTGC 3154
              |||| || || ||| |
Db        266 TGAGGGCCTGATCTTC 251


RESULT 6
US-09-916-204-3
; Sequence 3, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
;  APPLICANT: WEI, Ming-Hui et al.
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001164CIP
;  CURRENT APPLICATION NUMBER: US/09/916,204
;  CURRENT FILING DATE:  2001-07-24
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 48763
;   TYPE: DNA
;   ORGANISM: Human
US-09-916-204-3

  Query Match             2.6%;  Score 82.6;  DB 4;  Length 48763;
  Best Local Similarity   72.2%;  Pred. No. 4.2e-15;
  Matches  135;  Conservative    0;  Mismatches   49;  Indels    3;  Gaps    2;

Qy       3000 AATGGTTTGTTTCAGTCAGTTTAGGCTGCTATAAGAGAATATCTTAGAGTGGGTAATCTA 3059
              ||  ||   | | |||| |||| |||||| |||| || ||| |||||| | || ||| ||
Db      15209 AAACGTGCATCTGAGTCTGTTTGGGCTGCGATAATAG-ATACCTTAGACTTGGCAATTTA 15267

Qy       3060 TCAGCAATAGGAATTTATTGTTCACAATTCTGGAGGCTGGAAAATCCAAGATCAAGGCTC 3119
              | | |||||| |||| |||| | ||| || || | ||||| || |||||||||||||| |
Db      15268 TAAACAATAGAAATTCATTGCTGACAGTTGTGAAGACTGGGAAGTCCAAGATCAAGGCGC 15327

Qy       3120 CAGCAGGTTCAGTGTCTGCTGAGTGCTTGTTCTGCTTCGAAGATGGCACCTTTTTGCTGT 3179
              ||||   |   || |||| |||  |||    ||||||| || ||||| |||| ||||||
Db      15328 CAGCGAATCTGGTATCTGGTGATGGCT--CCCTGCTTCAAAAATGGCGCCTTCTTGCTGC 15385

Qy       3180 GTTCTCA 3186
               |  |||
Db      15386 ATCTTCA 15392


RESULT 7
US-09-804-471A-3
; Sequence 3, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001164
;  CURRENT APPLICATION NUMBER: US/09/804,471A
;  CURRENT FILING DATE:  2001-03-13
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 174493
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(174493)
;   OTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3

  Query Match             2.6%;  Score 82.6;  DB 4;  Length 174493;
  Best Local Similarity   72.2%;  Pred. No. 1.1e-14;
  Matches  135;  Conservative    0;  Mismatches   49;  Indels    3;  Gaps    2;

Qy        3000 AATGGTTTGTTTCAGTCAGTTTAGGCTGCTATAAGAGAATATCTTAGAGTGGGTAATCTA 3059
               ||  ||   | | |||| |||| |||||| |||| || ||| |||||| | || ||| ||
Db       14097 AAACGTGCATCTGAGTCTGTTTGGGCTGCGATAATAG-ATACCTTAGACTTGGCAATTTA 14155

Qy        3060 TCAGCAATAGGAATTTATTGTTCACAATTCTGGAGGCTGGAAAATCCAAGATCAAGGCTC 3119
               | | |||||| |||| |||| | ||| || || || |||| || |||||||||||||| |
Db       14156 TAAACAATAGAAATTCATTGCTGACAGTTGTGAAGACTGGGAAGTCCAAGATCAAGGCGC 14215

Qy        3120 CAGCAGGTTCAGTGTCTGCTGAGTGCTTGTTCTGCTTCGAAGATGGCACCTTTTTGCTGT 3179
               ||||   |   || |||| |||  |||    ||||||| || ||||| |||| ||||||
Db       14216 CAGCGAATCTGGTATCTGGTGATGGCT--CCCTGCTTCAAAAATGGCGCCTTCTTGCTGC 14273

Qy        3180 GTTCTCA 3186
                |  |||
Db       14274 ATCTTCA 14280

RESULT 8
US-10-238-709-3
; Sequence 3, Application US/10238709
; Patent No. 6680188
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001164DIV
;  CURRENT APPLICATION NUMBER: US/10/238,709
;  CURRENT FILING DATE:  2002-09-11
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 174493
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(174493)
;   OTHER INFORMATION: n = A,T,C or G
US-10-238-709-3

  Query Match             2.6%;  Score 82.6;  DB 4;  Length 174493;
  Best Local Similarity   72.2%;  Pred. No. 1.1e-14;
  Matches  135;  Conservative    0;  Mismatches   49;  Indels    3;  Gaps    2;

Qy        3000 AATGGTTTGTTTCAGTCAGTTTAGGCTGCTATAAGAGAATATCTTAGAGTGGGTAATCTA 3059
               ||  ||   | | |||| |||| |||||| |||| || ||| |||||| | || ||| ||
Db       14097 AAACGTGCATCTGAGTCTGTTTGGGCTGCGATAATAG-ATACCTTAGACTTGGCAATTTA 14155

Qy        3060 TCAGCAATAGGAATTTATTGTTCACAATTCTGGAGGCTGGAAAATCCAAGATCAAGGCTC 3119
               | | |||||| |||| |||| | ||| || || || |||| || |||||||||||||| |
Db       14156 TAAACAATAGAAATTCATTGCTGACAGTTGTGAAGACTGGGAAGTCCAAGATCAAGGCGC 14215

Qy        3120 CAGCAGGTTCAGTGTCTGCTGAGTGCTTGTTCTGCTTCGAAGATGGCACCTTTTTGCTGT 3179
               ||||   |   || |||| |||  |||    ||||||| || ||||| |||| ||||||
Db       14216 CAGCGAATCTGGTATCTGGTGATGGCT--CCCTGCTTCAAAAATGGCGCCTTCTTGCTGC 14273

Qy        3180 GTTCTCA 3186
                |  |||
Db       14274 ATCTTCA 14280

RESULT 9
```

```
US-09-497-855A-40/c
; Sequence 40, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
;  APPLICANT: Huang, Tim
;  TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
;  FILE REFERENCE: UMO1523
;  CURRENT APPLICATION NUMBER: US/09/497,855A
;  CURRENT FILING DATE:  2000-02-04
;  PRIOR APPLICATION NUMBER: 60/120,592
;  PRIOR FILING DATE: 1999-02-18
;  PRIOR APPLICATION NUMBER: 60/118,760
;  PRIOR FILING DATE: 1999-02-05
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
;   LENGTH: 161652
;   TYPE: DNA
;   ORGANISM: Homo sapiens;
US-09-497-855A-40

  Query Match             2.6%;  Score 82.2;  DB 4;  Length 161652;
  Best Local Similarity   69.6%;  Pred. No. 1.4e-14;
  Matches  126;  Conservative    0;  Mismatches   53;  Indels    2;  Gaps    1;

Qy        3007 TGTTTCAGTCAGTTTAGGCTGCTATAAGAGAATATCTTAGAGTGGGTAATCTATCAGCAA 3066
               ||| |  |||  |||  |||||||||| | |||| |  ||  |||||||| ||| |  |
Db       13993 TGTCTTGGTCTATTTGTGCTGCTATAACAAAATACCCAAGCCTGGGTAATTTATAAAAAG 13934

Qy        3067 TAGGAATTTATTGTTCACAATTCTGGAGGCTGGAAAATCCAAGATCAAGGCTCCAGCAGG 3126
                || |||||| |  ||| | ||||||||||||| || | ||| | ||| || | |||| |
Db       13933 CAGAAATTTAGTTCTCATAGTTCTGGAGGCTGGGAAGTTCAAAACCAAAGCACTAGCAAG 13874

Qy        3127 TTCAGTGTCTGCTGAGTG--CTTGTTCTGCTTCGAAGATGGCACCTTTTTGCTGTGTTCT 3184
               ||  |||||||   || |  ||   |||||||| ||||| |   ||| ||||||  | ||
Db       13873 TTTTGTGTCTGGATAGGGCCCTGTGTCTGCTTCCAAGATAGTGACTTGTTGCTGCATCCT 13814

Qy        3185 C 3185
               |
Db       13813 C 13813

RESULT 10
US-09-873-404-3
; Sequence 3, Application US/09873404
; Patent No. 6500656
; GENERAL INFORMATION:
;  APPLICANT: WEBSTER, Marion et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001212-CIP
;  CURRENT APPLICATION NUMBER: US/09/873,404
;  CURRENT FILING DATE:  2001-06-05
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 63588
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(63588)
;   OTHER INFORMATION: n = A,T,C or G
US-09-873-404-3

  Query Match             2.5%;  Score 80.8;  DB 4;  Length 63588;
  Best Local Similarity   71.6%;  Pred. No. 2e-14;
  Matches  106;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy        2999 AAATGGTTTGTTTCAGTCAGTTTAGGCTGCTATAAGAGAATATCTTAGAGTGGGTAATCT 3058
               ||||  | ||||| ||||  ||   || ||||||| | |||| | || | | |||    |
Db       15658 AAATCATCTGTTTTAGTCTATTCCAGCAGCTATAACAAAATACCATAAACTAGGTGGCTT 15717
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Qy       3059 ATCAGCAATAGGAATTTATTGTTCACAATTCTGGAGGCTGGAAAATCCAAGATCAAGGCT 3118
              || | ||  || ||||||||  |  || ||||||||||||| || | |||||||||||
Db      15718 ATAAACAGCAGAAATTTATTTCTGGCAGTTCTGGAGGCTGGGAAGTGCAAGATCAAGGTG 15777

Qy       3119 CCAGCAGGTTCAGTGTCTGCTGAGTGCT 3146
              |  |||| ||||||||||| |||| | |
Db      15778 CAGGCAGATTCAGTGTCTGGTGAGGGTT 15805

RESULT 11
US-09-146-053-4
; Sequence 4, Application US/09146053A
; Patent No. 6399349
; GENERAL INFORMATION:
;  APPLICANT: Ryan, James W.
;  APPLICANT: Sprinkle, Terry Joe Curtis
;  APPLICANT: Venema, Richard C.
;  TITLE OF INVENTION: Human Aminopeptidase P Gene
;  FILE REFERENCE: MCG103
;  CURRENT APPLICATION NUMBER: US/09/146,053A
;  CURRENT FILING DATE: 1998-09-02
;  EARLIER APPLICATION NUMBER: 60/057,854
;  EARLIER FILING DATE: 1997-09-02
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 50000
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-146-053-4

  Query Match             2.5%;  Score 80.4;  DB 4;  Length 50000;
  Best Local Similarity   68.7%;  Pred. No. 2.3e-14;
  Matches  125;  Conservative    0;  Mismatches   56;  Indels    1;  Gaps    1;

Qy       3005 TTTGTTTCAGTCAGTTTAGGCTGCTATAAGAGAATATCTTAGAGTGGGTAATCTATCAGC 3064
              ||| | | ||||  ||  ||||||||||| | |       ||| ||| |    ||| | |
Db      37896 TTTATCTTAGTCCATTGGGGCTGCTATAACAAAGGCCTGCAGACTGGTTGGCTTATAAAC 37955

Qy       3065 AATAGGAATTTATTGTTCACAATTCTGGAGGCTGGAAAATCCAAGATCAAGGCTCCAGCA 3124
              | |||  |||||||  | ||| ||||||||||||| || || ||||||||||| | ||||
Db      37956 AGTAGACATTTATTTCTTACAGTTCTGGAGGCTGGGAAGTCGAAGATCAAGGCACTAGCA 38015

Qy       3125 GGTTCAGTGTCTGCTGAGTGCTTGTTCTGCTTCGAAGATGGCACCTTTTTGCTGTGTTCT 3184
              | ||  |||||     || ||    | | ||||| |||||||||||  | ||||| | ||
Db      38016 GATTTGGTGTCCAACAAGGGCCCAGT-TCCTTCGTAGATGGCACCTCCTAGCTGTATCCT 38074

Qy       3185 CA 3186
              ||
Db      38075 CA 38076

RESULT 12
US-09-497-855A-37
; Sequence 37, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
;  APPLICANT: Huang, Tim
;  TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
;  FILE REFERENCE: UMO1523
;  CURRENT APPLICATION NUMBER: US/09/497,855A
;  CURRENT FILING DATE:  2000-02-04
;  PRIOR APPLICATION NUMBER: 60/120,592
;  PRIOR FILING DATE: 1999-02-18
;  PRIOR APPLICATION NUMBER: 60/118,760
;  PRIOR FILING DATE: 1999-02-05
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
;   LENGTH: 193303
;   TYPE: DNA
;   ORGANISM: Homo sapiens;
```

```
US-09-497-855A-37

  Query Match             2.5%;  Score 79.2;  DB 4;  Length 193303;
  Best Local Similarity   66.3%;  Pred. No. 1.5e-13;
  Matches  114;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy       3015 TCAGTTTAGGCTGCTATAAGAGAATATCTTAGAGTGGGTAATCTATCAGCAATAGGAATT 3074
              ||||| |  ||  |||||| | ||   |  |      |  |  ||  |  ||||||||||
Db      61650 TCAGTCTGTGCCACTATAACAAAAATACCCAAGACTAGGCAATTAATAAGAATAGGAATT 61709

Qy       3075 TATTGTTCACAATTCTGGAGGCTGGAAAATCCAAGATCAAGGCTCCAGCAGGTTCAGTGT 3134
              ||||    || |||||||||||||| || |||||||||||||| |||| ||  || ||||
Db      61710 TATTCCATACCATTCTGGAGGCTGGGAAGTCCAAGATCAAGGCACCAGTAGAGTCTGTGT 61769

Qy       3135 CTGCTGAGTGCTTGTTCTGCTTCGAAGATGGCACCTTTTTGCTGTGTTCTCA 3186
               ||            |||||||| |||| || ||||| ||||||  | ||||
Db      61770 TTGTGACAACTGCTGTCTGCTTCCAAGACGGTACCTTGTTGCTGCATCCTCA 61821

RESULT 13
US-09-497-855A-44
; Sequence 44, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
;  APPLICANT: Huang, Tim
;  TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
;  FILE REFERENCE: UMO1523
;  CURRENT APPLICATION NUMBER: US/09/497,855A
;  CURRENT FILING DATE:  2000-02-04
;  PRIOR APPLICATION NUMBER: 60/120,592
;  PRIOR FILING DATE: 1999-02-18
;  PRIOR APPLICATION NUMBER: 60/118,760
;  PRIOR FILING DATE: 1999-02-05
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
;   LENGTH: 193303
;   TYPE: DNA
;   ORGANISM: Homo sapiens;
US-09-497-855A-44

  Query Match             2.5%;  Score 79.2;  DB 4;  Length 193303;
  Best Local Similarity   66.3%;  Pred. No. 1.5e-13;
  Matches  114;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy       3015 TCAGTTTAGGCTGCTATAAGAGAATATCTTAGAGTGGGTAATCTATCAGCAATAGGAATT 3074
              ||||| |  ||  |||||| | ||   |  |      |  |  ||  |  ||||||||||
Db      61650 TCAGTCTGTGCCACTATAACAAAAATACCCAAGACTAGGCAATTAATAAGAATAGGAATT 61709

Qy       3075 TATTGTTCACAATTCTGGAGGCTGGAAAATCCAAGATCAAGGCTCCAGCAGGTTCAGTGT 3134
              ||||    || |||||||||||||| || |||||||||||||| |||| ||  || ||||
Db      61710 TATTCCATACCATTCTGGAGGCTGGGAAGTCCAAGATCAAGGCACCAGTAGAGTCTGTGT 61769

Qy       3135 CTGCTGAGTGCTTGTTCTGCTTCGAAGATGGCACCTTTTTGCTGTGTTCTCA 3186
               ||            |||||||| |||| || ||||| ||||||  | ||||
Db      61770 TTGTGACAACTGCTGTCTGCTTCCAAGACGGTACCTTGTTGCTGCATCCTCA 61821

RESULT 14
US-09-671-317-212
; Sequence 212, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Cohen, Annick
;  TITLE OF INVENTION:  BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
;  FILE REFERENCE:  62.US3.CIP
;  CURRENT APPLICATION NUMBER: US/09/671,317
;  CURRENT FILING DATE:  2000-09-27
;  PRIOR APPLICATION NUMBER:  US 09/536,178
;  PRIOR FILING DATE:  2000-03-23
;  PRIOR APPLICATION NUMBER:  PCT/IB00/00403
;  PRIOR FILING DATE:  2000-03-24
;  PRIOR APPLICATION NUMBER:  US 60/126,269
;  PRIOR FILING DATE:  1999-03-25
;  PRIOR APPLICATION NUMBER:  US 60/131,961
;  PRIOR FILING DATE:  1999-04-30
;  NUMBER OF SEQ ID NOS:  977
;  SOFTWARE:  Patent.pm
; SEQ ID NO 212
;   LENGTH: 1001
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 501
;   OTHER INFORMATION: 12-500-220 : polymorphic base A or G
;   NAME/KEY: misc_binding
;   LOCATION: 481..500
;   OTHER INFORMATION: 12-500-220.mis1, potential
;   NAME/KEY: misc_binding
;   LOCATION: 502..521
;   OTHER INFORMATION: 12-500-220.mis2, potential complement
;   NAME/KEY: primer_bind
;   LOCATION: 283..303
;   OTHER INFORMATION: upstream amplification primer
;   NAME/KEY: primer_bind
;   LOCATION: 711..731
;   OTHER INFORMATION: downstream amplification primer, complement
;   NAME/KEY: misc_binding
;   LOCATION: 489..513
;   OTHER INFORMATION: 12-500-220 potential probe
US-09-671-317-212

  Query Match             2.5%;  Score 79;  DB 4;  Length 1001;
  Best Local Similarity   75.5%;  Pred. No. 3.7e-15;
  Matches  111;  Conservative    0;  Mismatches   35;  Indels    1;  Gaps    1;

Qy       3007 TGTTTCAGTCAGTTTAGGCTGCTATAAGA-GAATATCTTAGAGTGGGTAATCTATCAGCA 3065
              ||| |  ||  |||| ||||||| ||| |  |||| |||| |||||||    ||| | ||
Db        837 TGTCTTGGTTTGTTTGGGCTGCTGTAACAAAAATACCTTACAGTGGGTGGCTTATAAACA 896

Qy       3066 ATAGGAATTTATTGTTCACAATTCTGGAGGCTGGAAAATCCAAGATCAAGGCTCCAGCAG 3125
              | |||||| ||||| ||||| ||||||||||||| || | || ||||||| | || ||||
Db        897 ACAGGAATGTATTGCTCACAGTTCTGGAGGCTGGGAAGTTCACGATCAAGTCACCGGCAG 956

Qy       3126 GTTCAGTGTCTGCTGAGTGCTTGTTCT 3152
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Db        957 TTTCGGTGTGTGGTGAGAGCTTTTGCT 983


RESULT 15
US-09-671-317-458
; Sequence 458, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Cohen, Annick
;  TITLE OF INVENTION:  BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
;  FILE REFERENCE:  62.US3.CIP
;  CURRENT APPLICATION NUMBER: US/09/671,317
;  CURRENT FILING DATE:  2000-09-27
;  PRIOR APPLICATION NUMBER:  US 09/536,178
;  PRIOR FILING DATE:  2000-03-23
;  PRIOR APPLICATION NUMBER:  PCT/IB00/00403
;  PRIOR FILING DATE:  2000-03-24
;  PRIOR APPLICATION NUMBER:  US 60/126,269
;  PRIOR FILING DATE:  1999-03-25
;  PRIOR APPLICATION NUMBER:  US 60/131,961
;  PRIOR FILING DATE:  1999-04-30
;  NUMBER OF SEQ ID NOS:  977
;  SOFTWARE:  Patent.pm
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; SEQ ID NO 458
;   LENGTH: 1001
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 501
;   OTHER INFORMATION: 12-500-217 : insertion CAATA
;   NAME/KEY: misc_binding
;   LOCATION: 481..500
;   OTHER INFORMATION: 12-500-217.mis1, potential
;   NAME/KEY: primer_bind
;   LOCATION: 286..306
;   OTHER INFORMATION: upstream amplification primer
;   NAME/KEY: primer_bind
;   LOCATION: 714..734
;   OTHER INFORMATION: downstream amplification primer, complement
US-09-671-317-458

  Query Match             2.5%;  Score 79;  DB 4;  Length 1001;
  Best Local Similarity   75.5%;  Pred. No. 3.7e-15;
  Matches  111;  Conservative    0;  Mismatches   35;  Indels    1;  Gaps    1;

Qy       3007 TGTTTCAGTCAGTTTAGGCTGCTATAAGA-GAATATCTTAGAGTGGGTAATCTATCAGCA 3065
              ||| |  ||  |||| ||||||| ||| |  |||| |||| |||||||    ||| | ||
Db        840 TGTCTTGGTTTGTTTGGGCTGCTGTAACAAAAATACCTTACAGTGGGTGGCTTATAAACA 899

Qy       3066 ATAGGAATTTATTGTTCACAATTCTGGAGGCTGGAAAATCCAAGATCAAGGCTCCAGCAG 3125
              | |||||| ||||| ||||| ||||||||||||| || | || ||||||| | || ||||
Db        900 ACAGGAATGTATTGCTCACAGTTCTGGAGGCTGGGAAGTTCACGATCAAGTCACCGGCAG 959

Qy       3126 GTTCAGTGTCTGCTGAGTGCTTGTTCT 3152
               ||| |||| || |||| |||| | ||
Db        960 TTTCGGTGTGTGGTGAGAGCTTTTGCT 986


Search completed: June  8, 2004, 02:40:40
Job time : 200 secs
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                    GenCore version 5.1.6
             Copyright (c) 1993 - 2004  Compugen Ltd.

OM protein - protein search, using sw model

Run on:          June  7, 2004, 09:03:04 ; Search time 47 Seconds
                                          (without alignments)
                                          2340.498 Million cell updates/sec

Title:           US-09-900-448-2
Perfect score:   2185
Sequence:        1 MARVLGAPVALGLWSLCWSL..........NAAKALPQPQNVTSLLGCTH 391

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters:      1155919

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_AA:*
              1:  /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
              2:  /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
              3:  /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
              4:  /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
              5:  /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
              6:  /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
              7:  /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
              8:  /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
              9:  /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
              10:  /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
              11:  /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
              12:  /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
              13:  /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
              14:  /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
              15:  /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
              16:  /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
              17:  /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
              18:  /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                  SUMMARIES
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Result              Query
  No.    Score      Match Length DB  ID                         Description
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    1     2185      100.0    391  11  US-09-900-448-2           Sequence 2, Appli
    2   2139.5       97.9    462  11  US-09-900-448-4           Sequence 4, Appli
    3   1556.5       71.2    460  14  US-10-316-253-40          Sequence 40, Appl
    4     1338       61.2    255  15  US-10-162-335-88          Sequence 88, Appl
    5      258       11.8     87  11  US-09-864-408A-1100       Sequence 1100, Ap
    6      204        9.3    587  14  US-10-406-209-1           Sequence 1, Appli
    7    202.5        9.3    470  9  US-09-801-196-23          Sequence 23, Appl
    8    202.5        9.3    470  9  US-09-920-455-219         Sequence 219, App
    9    202.5        9.3    470  14  US-10-171-311-135         Sequence 135, App
   10    202.5        9.3    470  14  US-10-301-822-123         Sequence 123, App
   11    202.5        9.3    470  14  US-10-337-632-2           Sequence 2, Appli
   12    202.5        9.3    470  14  US-10-131-985-39          Sequence 39, Appl
   13    202.5        9.3    470  15  US-10-295-027-324         Sequence 324, App
   14    202.5        9.3    470  15  US-10-295-027-1243        Sequence 1243, Ap
   15    202.5        9.3    470  15  US-10-295-027-1244        Sequence 1244, Ap
   16    202.5        9.3    470  15  US-10-409-643-13          Sequence 13, Appl
   17    202.5        9.3    470  16  US-10-188-832-125         Sequence 125, App
   18    202.5        9.3    473  9  US-09-925-301-1217        Sequence 1217, Ap
   19      199        9.1    519  9  US-09-801-196-30          Sequence 30, Appl
   20      199        9.1    519  14  US-10-131-985-49          Sequence 49, Appl
   21      199        9.1    605  14  US-10-406-209-2           Sequence 2, Appli
   22      199        9.1    606  14  US-10-133-797-5           Sequence 5, Appli
   23      199        9.1    636  12  US-10-425-114-57113       Sequence 57113, A
   24      196        9.0    464  15  US-10-409-643-21          Sequence 21, Appl
   25    195.5        8.9    477  9  US-09-920-455-260         Sequence 260, App
   26    189.5        8.7    475  12  US-10-058-270A-78         Sequence 78, Appl
   27    189.5        8.7    475  15  US-10-295-027-8           Sequence 8, Appli
   28    189.5        8.7    476  9  US-09-801-196-25          Sequence 25, Appl
   29    189.5        8.7    476  12  US-10-211-462-10          Sequence 10, Appl
   30    189.5        8.7    476  14  US-10-021-660-72          Sequence 72, Appl
   31    189.5        8.7    476  14  US-10-131-985-35          Sequence 35, Appl
   32    189.5        8.7    476  16  US-10-188-832-4           Sequence 4, Appli
   33    183.5        8.4    467  9  US-09-801-196-20          Sequence 20, Appl
   34    183.5        8.4    467  10  US-09-759-130B-176        Sequence 176, App
   35    183.5        8.4    467  14  US-10-131-985-31          Sequence 31, Appl
   36    182.5        8.4    454  15  US-10-115-479-34          Sequence 34, Appl
   37    181.5        8.3    454  15  US-10-115-479-32          Sequence 32, Appl
   38    181.5        8.3    454  15  US-10-115-479-36          Sequence 36, Appl
   39    181.5        8.3    454  15  US-10-115-479-38          Sequence 38, Appl
   40    181.5        8.3    469  9  US-09-801-196-19          Sequence 19, Appl
   41    181.5        8.3    469  9  US-09-853-386-100         Sequence 100, App
   42    181.5        8.3    469  12  US-10-211-462-22          Sequence 22, Appl
   43    181.5        8.3    469  14  US-10-301-822-119         Sequence 119, App
   44    181.5        8.3    469  14  US-10-021-660-76          Sequence 76, Appl
   45    181.5        8.3    469  14  US-10-308-279-34          Sequence 34, Appl

                                 ALIGNMENTS

RESULT 1
US-09-900-448-2
; Sequence 2, Application US/09900448
; Publication No. US20030220488A1
; GENERAL INFORMATION:
;  APPLICANT: CECCARDI, Toni et al.
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001272
;  CURRENT APPLICATION NUMBER: US/09/900,448
;  CURRENT FILING DATE:  2001-07-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 391
;   TYPE: PRT
;   ORGANISM: Human
US-09-900-448-2

  Query Match             100.0%;  Score 2185;  DB 11;  Length 391;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-200;
  Matches  391;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MARVLGAPVALGLWSLCWSLAIATPLPPTSAHGNVAEGETKPDPDVTERCSDGWSFDATT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MARVLGAPVALGLWSLCWSLAIATPLPPTSAHGNVAEGETKPDPDVTERCSDGWSFDATT 60

Qy         61 LDDNGTMLFFKGEFVWKSHKWDRELISERWKNFPSPVDAAFRQGHNSVFLIKGDKVWVYP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LDDNGTMLFFKGEFVWKSHKWDRELISERWKNFPSPVDAAFRQGHNSVFLIKGDKVWVYP 120

Qy        121 PEKKEKGYPKLLQDEFPGIPSPLDAAVECHRGECQAEGVLFFQGHGHRNGTGHGNSTHHG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PEKKEKGYPKLLQDEFPGIPSPLDAAVECHRGECQAEGVLFFQGHGHRNGTGHGNSTHHG 180

Qy        181 PEYMRCSPHLVLSALTSDNHGATYAFSGTHYWRLDTSRDGWHSWPIAHQWPQGPSAVDAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PEYMRCSPHLVLSALTSDNHGATYAFSGTHYWRLDTSRDGWHSWPIAHQWPQGPSAVDAA 240

Qy        241 FSWEEKLYLVQGTQVYVFLTKGGYTLVSGYPKRLEKEVGTPHGIILDSVDAAFICPGSSR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FSWEEKLYLVQGTQVYVFLTKGGYTLVSGYPKRLEKEVGTPHGIILDSVDAAFICPGSSR 300

Qy        301 LHIMAGRRLWWLDLKSGAQATWTELPWPHEKVDGALCMEKSLGPNSCSANGPGLYLIHGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LHIMAGRRLWWLDLKSGAQATWTELPWPHEKVDGALCMEKSLGPNSCSANGPGLYLIHGP 360

Qy        361 NLYCYSDVEKLNAAKALPQPQNVTSLLGCTH 391
              |||||||||||||||||||||||||||||||
Db        361 NLYCYSDVEKLNAAKALPQPQNVTSLLGCTH 391


RESULT 2
US-09-900-448-4
; Sequence 4, Application US/09900448
; Publication No. US20030220488A1
; GENERAL INFORMATION:
;  APPLICANT: CECCARDI, Toni et al.
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001272
;  CURRENT APPLICATION NUMBER: US/09/900,448
;  CURRENT FILING DATE:  2001-07-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Human
US-09-900-448-4

  Query Match             97.9%;  Score 2139.5;  DB 11;  Length 462;
  Best Local Similarity   84.6%;  Pred. No. 3.1e-196;
  Matches  391;  Conservative    0;  Mismatches    0;  Indels   71;  Gaps    1;

Qy          1 MARVLGAPVALGLWSLCWSLAIATPLPPTSAHGNVAEGETKPDPDVTERCSDGWSFDATT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MARVLGAPVALGLWSLCWSLAIATPLPPTSAHGNVAEGETKPDPDVTERCSDGWSFDATT 60

Qy         61 LDDNGTMLFFKGEFVWKSHKWDRELISERWKNFPSPVDAAFRQGHNSVFLIKGDKVWVYP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LDDNGTMLFFKGEFVWKSHKWDRELISERWKNFPSPVDAAFRQGHNSVFLIKGDKVWVYP 120

Qy        121 PEKKEKGYPKLLQDEFPGIPSPLDAAVECHRGECQAEGVLFFQ----------------- 163
              |||||||||||||||||||||||||||||||||||||||||||
Db        121 PEKKEKGYPKLLQDEFPGIPSPLDAAVECHRGECQAEGVLFFQGDREWFWDLATGTMKER 180

Qy        164 ------------------------------------------------------GHGHRN 169
                                                                    ||||||
Db        181 SWPAVGNCSSALRWLGRYYCFQGNQFLRFDPVRGEVPPRYPRDVRDYFMPCPGRGHGHRN 240

Qy        170 GTGHGNSTHHGPEYMRCSPHLVLSALTSDNHGATYAFSGTHYWRLDTSRDGWHSWPIAHQ 229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGHGNSTHHGPEYMRCSPHLVLSALTSDNHGATYAFSGTHYWRLDTSRDGWHSWPIAHQ 300

Qy        230 WPQGPSAVDAAFSWEEKLYLVQGTQVYVFLTKGGYTLVSGYPKRLEKEVGTPHGIILDSV 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WPQGPSAVDAAFSWEEKLYLVQGTQVYVFLTKGGYTLVSGYPKRLEKEVGTPHGIILDSV 360

Qy        290 DAAFICPGSSRLHIMAGRRLWWLDLKSGAQATWTELPWPHEKVDGALCMEKSLGPNSCSA 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DAAFICPGSSRLHIMAGRRLWWLDLKSGAQATWTELPWPHEKVDGALCMEKSLGPNSCSA 420

Qy        350 NGPGLYLIHGPNLYCYSDVEKLNAAKALPQPQNVTSLLGCTH 391
              ||||||||||||||||||||||||||||||||||||||||||
Db        421 NGPGLYLIHGPNLYCYSDVEKLNAAKALPQPQNVTSLLGCTH 462


RESULT 3
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```
US-10-316-253-40
; Sequence 40, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
;  APPLICANT: The Procter & Gamble Company
;  APPLICANT:  Peters, Kevin
;  APPLICANT:  Thompson, Larry
;  APPLICANT:  Wang, Feng
;  APPLICANT:  Greis, Kenneth
;  TITLE OF INVENTION: Angiogenesis Modulating Proteins
;  FILE REFERENCE: 8865M
;  CURRENT APPLICATION NUMBER: US/10/316,253
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: US 60/355,295
;  PRIOR FILING DATE: 2002-02-08
;  NUMBER OF SEQ ID NOS: 308
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 460
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-10-316-253-40

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  Best Local Similarity   63.8%;  Pred. No. 2.5e-140;
  Matches  296;  Conservative   35;  Mismatches   54;  Indels   79;  Gaps    6;

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Db          1 MARTVVALNILVLLGLCWSLAVANPLP--AAHETVAKGENGTKPDSDVIEHCSDAWSFDA 58

Qy         59 TTLDDNGTMLFFKGEFVWKSHKWDRELISERWKNFPSPVDAAFRQGHNSVFLIKGDKVWV 118
              ||:| |||||||||||||: |   ||||||||||  : |||||| | :|||||| |||||
Db         59 TTMDHNGTMLFFKGEFVWRGHSGIRELISERWKNPVTSVDAAFR-GPDSVFLIKEDKVWV 117

Qy        119 YPPEKKEKGYPKLLQDEFPGIPSPLDAAVECHRGECQAEGVLFFQGH------------- 165
              ||||||| ||||| |:| |||| | ||||||||||||:||||||||:
Db        118 YPPEKKENGYPKLFQEESPGIPYPPDAAVECHRGECQSEGVLFFQGNRKWFWDFATRTQK 177

Qy        166 --------------------------------------------------------GH-- 167
                                                                      ||
Db        178 ERSWPAVGNCTAALRWLERYYCFQGNKFLRFNPVTGEVPPRYPLDARDYFISCPGRGHGK 237

Qy        168 -RNGTGHGNSTHHGPEYMRCSPHLVLSALTSDNHGATYAFSGTHYWRLDTSRDGWHSWPI 226
               |||| ||||||  | : ||:    |||| ||: ||||||||:||||||:||||||||||
Db        238 LRNGTAHGNSTH--PMHSRCNADPGLSALLSDHRGATYAFSGSHYWRLDSSRDGWHSWPI 295

Qy        227 AHQWPQGPSAVDAAFSWEEKLYLVQGTQVYVFLTKGGYTLVSGYPKRLEKEVGTPHGIIL 286
              || ||||||||||||||:||:||:|||||||||||||  ||||||||||||:|:| || |
Db        296 AHHWPQGPSAVDAAFSWDEKVYLIQGTQVYVFLTKGGNNLVSGYPKRLEKELGSPPGISL 355

Qy        287 DSVDAAFICPGSSRLHIMAGRRLWWLDLKSGAQATWTELPWPHEKVDGALCMEKSLGPNS 346
              |::|||| |||||:|:: :||||||||||||||||| || |||||||||||:|||||| |
Db        356 DTIDAAFSCPGSSKLYVTSGRRLWWLDLKSGAQATWAELSWPHEKVDGALCLEKSLGPYS 415

Qy        347 CSANGPGLYLIHGPNLYCYSDVEKLNAAKALPQPQNVTSLLGCT 390
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Db        416 CSSNGPNLFFIHGPNLYCYSSIDKLNAAKSLPQPQKVNSILGCS 459


RESULT 4
US-10-162-335-88
; Sequence 88, Application US/10162335
; Publication No. US20040009480A1
; GENERAL INFORMATION:
;  APPLICANT: Anderson, David W.
;  APPLICANT:  Baumgartner, Jason C.
;  APPLICANT:  Boldog, Ferenc L.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Hjalt, Tord
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Li, Li
;  APPLICANT:  MacDougall, John R.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Pena, Carol E. A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Stone, David J.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Vernet, Corine A. M.
;  APPLICANT:  Voss, Edward Z.
;  APPLICANT:  Zerhusen, Bryan D.
;  TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
;  FILE REFERENCE: 21402-377 B
;  CURRENT APPLICATION NUMBER: US/10/162,335
;  CURRENT FILING DATE:  2002-10-01
;  PRIOR APPLICATION NUMBER: 60/295,607
;  PRIOR FILING DATE: 2001-06-04
;  PRIOR APPLICATION NUMBER: 60/295,661
;  PRIOR FILING DATE: 2001-06-04
;  PRIOR APPLICATION NUMBER: 60/296,404
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: 60/296,418
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: 60/297,414
;  PRIOR FILING DATE: 2001-06-11
;  PRIOR APPLICATION NUMBER: 60/297,567
;  PRIOR FILING DATE: 2001-06-12
;  PRIOR APPLICATION NUMBER: 60/298,285
;  PRIOR FILING DATE: 2001-06-14
;  PRIOR APPLICATION NUMBER: 60/298,556
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/299,949
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/300,883
;  PRIOR FILING DATE: 2001-06-26
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 201
; SEQ ID NO 88
;   LENGTH: 255
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-162-335-88

  Query Match             61.2%;  Score 1338;  DB 15;  Length 255;
  Best Local Similarity   65.2%;  Pred. No. 1e-119;
  Matches  255;  Conservative    0;  Mismatches    0;  Indels  136;  Gaps    1;

Qy          1 MARVLGAPVALGLWSLCWSLAIATPLPPTSAHGNVAEGETKPDPDVTERCSDGWSFDATT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MARVLGAPVALGLWSLCWSLAIATPLPPTSAHGNVAEGETKPDPDVTERCSDGWSFDATT 60

Qy         61 LDDNGTMLFFKGEFVWKSHKWDRELISERWKNFPSPVDAAFRQGHNSVFLIKGDKVWVYP 120
              |||||||||||
Db         61 LDDNGTMLFFK------------------------------------------------- 71

Qy        121 PEKKEKGYPKLLQDEFPGIPSPLDAAVECHRGECQAEGVLFFQGHGHRNGTGHGNSTHHG 180

Db         72 ------------------------------------------------------------ 71

Qy        181 PEYMRCSPHLVLSALTSDNHGATYAFSGTHYWRLDTSRDGWHSWPIAHQWPQGPSAVDAA 240
                                         |||||||||||||||||||||||||||||||||
Db         72 ---------------------------GTHYWRLDTSRDGWHSWPIAHQWPQGPSAVDAA 104

Qy        241 FSWEEKLYLVQGTQVYVFLTKGGYTLVSGYPKRLEKEVGTPHGIILDSVDAAFICPGSSR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        105 FSWEEKLYLVQGTQVYVFLTKGGYTLVSGYPKRLEKEVGTPHGIILDSVDAAFICPGSSR 164

Qy        301 LHIMAGRRLWWLDLKSGAQATWTELPWPHEKVDGALCMEKSLGPNSCSANGPGLYLIHGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 LHIMAGRRLWWLDLKSGAQATWTELPWPHEKVDGALCMEKSLGPNSCSANGPGLYLIHGP 224

Qy        361 NLYCYSDVEKLNAAKALPQPQNVTSLLGCTH 391
              |||||||||||||||||||||||||||||||
Db        225 NLYCYSDVEKLNAAKALPQPQNVTSLLGCTH 255


RESULT 5
US-09-864-408A-1100
; Sequence 1100, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
;  APPLICANT: Leach, Martin D.
;  APPLICANT:  Shimkets, Richard A.
;  TITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides Encod
;  FILE REFERENCE: 21402-012
;  CURRENT APPLICATION NUMBER: US/09/864,408A
;  CURRENT FILING DATE:  2001-05-24
;  PRIOR APPLICATION NUMBER: 60/206,690
;  PRIOR FILING DATE: 2000-05-24
;  NUMBER OF SEQ ID NOS: 9068
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1100
;   LENGTH: 87
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: Wherein Xaa may be any naturally occuring amino acid
US-09-864-408A-1100

  Query Match             11.8%;  Score 258;  DB 11;  Length 87;
  Best Local Similarity   86.5%;  Pred. No. 8.8e-17;
  Matches   45;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        114 DKVWVYPPEKKEKGYPKLLQDEFPGIPSPLDAAVECHRGECQAEGVLFFQGH 165
              |||||||||||| ||||| |:|||||| | ||||||||||||:||||||||:
Db          5 DKVWVYPPEKKENGYPKLFQEEFPGIPYPPDAAVECHRGECQSEGVLFFQGN 56


RESULT 6
US-10-406-209-1
; Sequence 1, Application US/10406209
; Publication No. US20030170758A1
; GENERAL INFORMATION:
;  APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
;  TITLE OF INVENTION: NOVEL ANTIBODIES, DRUGS CONTAINING THESE ANTIBODIES AND
;  TITLE OF INVENTION:  METHODS FOR
;  TITLE OF INVENTION:  SCREENING COMPOUNDS BY USING THESE ANTIBODIES
;  FILE REFERENCE: 1241.19
;  CURRENT APPLICATION NUMBER: US/10/406,209
;  CURRENT FILING DATE:  2003-04-04
;  PRIOR APPLICATION NUMBER: US/09/806,228C
;  PRIOR FILING DATE: 2001-08-30
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/JP99/05350
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 10-291501
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 10-291503
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-29
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 587
;   TYPE: PRT
;   ORGANISM: Mouse
US-10-406-209-1

  Query Match              9.3%;  Score 204;  DB 14;  Length 587;
  Best Local Similarity   24.4%;  Pred. No. 1.8e-10;
  Matches  103;  Conservative   34;  Mismatches  127;  Indels  158;  Gaps   25;

Qy          5 LGAPVALGL--------WSLCWSLAIATPL----------PPTSAHGNVAEGETKPDPDV 46
              :| ||  ||        | |       :|           ||           | |  ||
Db        273 VGDPVRYGLPYEDRVRVWQLYGVRESVSPTAQLDTPEPEEPPLLPEPPNNRSSTPPQKDV 332

Qy         47 TERCSDGWSFDATTLDDNGTMLFFKGEFVWKSHKWDRELISER-------WKNFP---SP 96
                ||:    |||      |   ||||:: |:  : || |:| :       |:  |
Db        333 PHRCTA--HFDAVA-QIRGEAFFFKGKYFWRLTR-DRHLVSLQPAQMHRFWRGLPLHLDS 388

Qy         97 VDAAF-RQGHNSVFLIKGDKVWVYPPEKKEKGYPKLLQDEFPGIPSPLDAAVECHRGECQ 155
              ||| : |   : :   |||: ||:     |:|| : : | |   |  :||
Db        389 VDAVYERTSDHKIVFFKGDRYWVFKDNNVEEGYPRPVSD-FSLPPGGIDA---------- 437

Qy        156 AEGVLFFQGHGHRNGTGHGNSTHHGPEYMRCSPHLVLSALTSDNHGATYAFSGTHYWRLD 215
                  :|   |  |                                  || |    ||| |
Db        438 ----VFSWAHNDR----------------------------------TYFFKDQLYWRYD 459

Qy        216 --TSR--DGWHS-WPIAHQWPQGPSAVDAAFSWEE-KLYLVQGTQVYVFLTKGGYTLVSG 269
                | |   |: :  |:   |   || :| |  | :   |  :| | |  :  |      |
Db        460 DHTRRMDPGYPAQGPL---WRGVPSMLDDAMRWSDGASYFFRG-QSYWKVLDGELEAAPG 515

Qy        270 YPKRLEKE---VGTPHGIILDSVDAAFICPGSSRLHIMAGRRLWWLDLKSGAQATWTELP 326
              ||:   ::    | |        ||  : ||        ||        ||||
Db        516 YPQSTARDWLVCGEP------LADAEDVGPGPQ------GR--------SGAQ------- 548

Qy        327 WPHEKVDG-ALCMEKSLGPNSCSANGPGLYLIHGPNLYCYSDVEKLNAAKALPQPQNVTS 385
                    || |:|                          | ||  :|    |||    :|
Db        549 ------DGLAVCS-------------------------CTSDAHRL----ALPSLLLLTP 573

Qy        386 LL 387
              ||
Db        574 LL 575

RESULT 7
US-09-801-196-23
; Sequence 23, Application US/09801196
; Patent No. US20020037827A1
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Kai
;  APPLICANT:  Smith, Ryan
;  APPLICANT:  Fajardo, Mark
;  APPLICANT:  Mcss, Patrick
;  TITLE OF INVENTION:  A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
;  TITLE OF INVENTION:  EXPRESSED IN SKIN CELLS
;  FILE REFERENCE:  240083.509
;  CURRENT APPLICATION NUMBER: US/09/801,196
;  CURRENT FILING DATE:  2001-03-06
;  NUMBER OF SEQ ID NOS:  37
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-801-196-23

  Query Match             9.3%;  Score 202.5;  DB 9;  Length 470;
  Best Local Similarity   27.3%;  Pred. No. 1.9e-10;
  Matches   66;  Conservative   23;  Mismatches   90;  Indels   63;  Gaps   10;

Qy         30 SAHGNVAEGETKPDPDVTE--RCSDGWSFDATTLDDNGTMLFFKGEFVW----KSHKWDR 83
              | :|:  | :  |:|| :|   |    |||| |   |  : |||  | |    :  |
Db        260 SLYGDPKENQRLPNPDNSEPALCDPNLSFDAVTTVGN-KIFFFKDRFFWLKVSERPKTSV 318

Qy         84 ELISERWKNFPSPVDAAFR-QGHNSVFLIKGDKVWVYPPEKKEKGYPKLLQD-EFPGIPS 141
               |||  |   || ::||:  :  | ||| | || |:    : |  ||| :    ||
Db        319 NLISSLWPTLPSGIEAAYEIEARNQVFLFKDDKYWLISNLRPEPNYPKSIHSFGFPNFVK 378

Qy        142 PLDAAVECHRGECQAEGVLFFQGHGHRNGTGHGNSTHHGPEYMRCSPHLVLSALTSDNHG 201
               :||||                                 | : |
Db        379 KIDAAV-------------------------------FNPRFYR---------------- 391
```

```
Qy        202 ATYAFSGTHYWRLDTSRD----GWHSWPIAHQWPQGPSAVDAAFSWEEK-LYLVQGTQVY 256
               || |    ||| |  |     |:      :    ||  :|| |  : |  |  ||:  :
Db        392 -TYFFVDNQYWRYDERRQMMDPGYPKLITKNFQGIGPK-IDAVFYSKNKYYYFFQGSNQF 449

Qy        257 VF 258
               :
Db        450 EY 451

RESULT 8
US-09-920-455-219
; Sequence 219, Application US/09920455
; Patent No. US20020168647A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Fan, Liqun
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF HEAD AND NECK CANCER
;  FILE REFERENCE: 210121.540
;  CURRENT APPLICATION NUMBER: US/09/920,455
;  CURRENT FILING DATE:  2001-08-01
;  NUMBER OF SEQ ID NOS: 275
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 219
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-920-455-219

  Query Match             9.3%;  Score 202.5;  DB 9;  Length 470;
  Best Local Similarity   27.3%;  Pred. No. 1.9e-10;
  Matches   66;  Conservative   23;  Mismatches   90;  Indels   63;  Gaps   10;

Qy         30 SAHGNVAEGETKPDPDVTE--RCSDGWSFDATTLDDNGTMLFFKGEFVW----KSHKWDR 83
              | :|:  | :  |:|| :|   |    |||| |   |  : |||  | |    :  |
Db        260 SLYGDPKENQRLPNPDNSEPALCDPNLSFDAVTTVGN-KIFFFKDRFFWLKVSERPKTSV 318

Qy         84 ELISERWKNFPSPVDAAFR-QGHNSVFLIKGDKVWVYPPEKKEKGYPKLLQD-EFPGIPS 141
               |||  |   || ::||:  :  | ||| | || |:    : |  ||| :    ||
Db        319 NLISSLWPTLPSGIEAAYEIEARNQVFLFKDDKYWLISNLRPEPNYPKSIHSFGFPNFVK 378

Qy        142 PLDAAVECHRGECQAEGVLFFQGHGHRNGTGHGNSTHHGPEYMRCSPHLVLSALTSDNHG 201
               :||||                                 | : |
Db        379 KIDAAV-------------------------------FNPRFYR---------------- 391

Qy        202 ATYAFSGTHYWRLDTSRD----GWHSWPIAHQWPQGPSAVDAAFSWEEK-LYLVQGTQVY 256
               || |    ||| |  |     |:      :    ||  :|| |  : |  |  ||:  :
Db        392 -TYFFVDNQYWRYDERRQMMDPGYPKLITKNFQGIGPK-IDAVFYSKNKYYYFFQGSNQF 449

Qy        257 VF 258
               :
Db        450 EY 451

RESULT 9
US-10-171-311-135
; Sequence 135, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
;  APPLICANT: Schlegel, Robert
;  APPLICANT:  Chen, Yan
;  APPLICANT:  Zhao, Xumei
;  APPLICANT:  Monahan, John
;  APPLICANT:  Kamatkar, Shubhangi
;  APPLICANT:  Glatt, Karen
;  APPLICANT:  Gannavarapu, Manjula
;  APPLICANT:  Hoersh, Sebastian
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
;  TITLE OF INVENTION:  OF CERVICAL CANCER
;  FILE REFERENCE: MRI-035
;  CURRENT APPLICATION NUMBER: US/10/171,311
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: US 60/298,159
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,155
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/335,936
;  PRIOR FILING DATE: 2001-11-14
;  NUMBER OF SEQ ID NOS: 238
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 135
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-171-311-135

  Query Match             9.3%;  Score 202.5;  DB 14;  Length 470;
  Best Local Similarity   27.3%;  Pred. No. 1.9e-10;
  Matches   66;  Conservative   23;  Mismatches   90;  Indels   63;  Gaps   10;

Qy          30 SAHGNVAEGETKPDPDVTE--RCSDGWSFDATTLDDNGTMLFFKGEFVW----KSHKWDR 83
               | :|:  | :  |:|| :|   |    |||| |   |  : |||  | |    :  |
Db         260 SLYGDPKENQRLPNPDNSEPALCDPNLSFDAVTTVGN-KIFFFKDRFFWLKVSERPKTSV 318

Qy          84 ELISERWKNFPSPVDAAFR-QGHNSVFLIKGDKVWVYPPEKKEKGYPKLLQD-EFPGIPS 141
                |||  |   || ::||:  :  | ||| | || |:    : |  ||| :    ||
Db         319 NLISSLWPTLPSGIEAAYEIEARNQVFLFKDDKYWLISNLRPEPNYPKSIHSFGFPNFVK 378

Qy         142 PLDAAVECHRGECQAEGVLFFQGHGHRNGTGHGNSTHHGPEYMRCSPHLVLSALTSDNHG 201
                :||||                                 | : |
Db         379 KIDAAV-------------------------------FNPRFYR---------------- 391

Qy         202 ATYAFSGTHYWRLDTSRD----GWHSWPIAHQWPQGPSAVDAAFSWEEK-LYLVQGTQVY 256
                || |    ||| |  |     |:      :    ||  :|| |  : |  |  ||:  :
Db         392 -TYFFVDNQYWRYDERRQMMDPGYPKLITKNFQGIGPK-IDAVFYSKNKYYYFFQGSNQF 449

Qy         257 VF 258
                :
Db         450 EY 451

RESULT 10
US-10-301-822-123
; Sequence 123, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc.
;  APPLICANT:  Berger, Allison
;  APPLICANT:  Guillemette, Tracy L.
;  APPLICANT:  Kamatkar, Shubhangi
;  APPLICANT:  Schlegel, Robert
;  APPLICANT:  Monahan, John E.
;  APPLICANT:  Thibodeau, Stephen N.
;  APPLICANT:  Burgart, Lawrence J.
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
;  TITLE OF INVENTION:  METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;  TITLE OF INVENTION:  THERAPY OF COLON CANCER
;  FILE REFERENCE: MPM01-029P2RNM
;  CURRENT APPLICATION NUMBER: US/10/301,822
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 60/339,971
;  PRIOR FILING DATE: 2001-12-10
;  PRIOR APPLICATION NUMBER: US 60/361,978
;  PRIOR FILING DATE: 2002-03-05
;  PRIOR APPLICATION NUMBER: US 60/381,988
;  PRIOR FILING DATE: 2002-05-20
;  NUMBER OF SEQ ID NOS: 228
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 123
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-301-822-123

  Query Match             9.3%;  Score 202.5;  DB 14;  Length 470;
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  Best Local Similarity   27.3%;  Pred. No. 1.9e-10;
  Matches   66;  Conservative   23;  Mismatches   90;  Indels   63;  Gaps   10;

Qy          30 SAHGNVAEGETKPDPDVTE--RCSDGWSFDATTLDDNGTMLFFKGEFVW----KSHKWDR 83
               | :|:  | :  |:|| :|   |    |||| |   |  : |||  | |    :  |
Db         260 SLYGDPKENQRLPNPDNSEPALCDPNLSFDAVTTVGN-KIFFFKDRFFWLKVSERPKTSV 318

Qy          84 ELISERWKNFPSPVDAAFR-QGHNSVFLIKGDKVWVYPPEKKEKGYPKLLQD-EFPGIPS 141
                |||  |   || ::||:  :  | ||| | || |:    : |  ||| :    ||
Db         319 NLISSLWPTLPSGIEAAYEIEARNQVFLFKDDKYWLISNLRPEPNYPKSIHSFGFPNFVK 378

Qy         142 PLDAAVECHRGECQAEGVLFFQGHGHRNGTGHGNSTHHGPEYMRCSPHLVLSALTSDNHG 201
                :||||                                 | : |
Db         379 KIDAAV-------------------------------FNPRFYR---------------- 391

Qy         202 ATYAFSGTHYWRLDTSRD----GWHSWPIAHQWPQGPSAVDAAFSWEEK-LYLVQGTQVY 256
                || |    ||| |  |     |:      :    ||  :|| |  : |  |  ||:  :
Db         392 -TYFFVDNQYWRYDERRQMMDPGYPKLITKNFQGIGPK-IDAVFYSKNKYYYFFQGSNQF 449

Qy         257 VF 258
                :
Db         450 EY 451

RESULT 11
US-10-337-632-2
; Sequence 2, Application US/10337632
; Publication No. US20030157110A1
; GENERAL INFORMATION:
;  APPLICANT: An, Frank
;  APPLICANT:  Chen, Hong
;  TITLE OF INVENTION: METHODS FOR THE TREATMENT OF METABOLIC
;  TITLE OF INVENTION:  DISORDERS, INCLUDING OBESITY AND DIABETES
;  FILE REFERENCE: MPI01-253P1RM
;  CURRENT APPLICATION NUMBER: US/10/337,632
;  CURRENT FILING DATE:  2003-01-07
;  PRIOR APPLICATION NUMBER: 60/346,354
;  PRIOR FILING DATE: 2002-01-07
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-337-632-2

  Query Match             9.3%;  Score 202.5;  DB 14;  Length 470;
  Best Local Similarity   27.3%;  Pred. No. 1.9e-10;
  Matches   66;  Conservative   23;  Mismatches   90;  Indels   63;  Gaps   10;

Qy          30 SAHGNVAEGETKPDPDVTE--RCSDGWSFDATTLDDNGTMLFFKGEFVW----KSHKWDR 83
               | :|:  | :  |:|| :|   |    |||| |   |  : |||  | |    :  |
Db         260 SLYGDPKENQRLPNPDNSEPALCDPNLSFDAVTTVGN-KIFFFKDRFFWLKVSERPKTSV 318

Qy          84 ELISERWKNFPSPVDAAFR-QGHNSVFLIKGDKVWVYPPEKKEKGYPKLLQD-EFPGIPS 141
                |||  |   || ::||:  :  | ||| | || |:    : |  ||| :    ||
Db         319 NLISSLWPTLPSGIEAAYEIEARNQVFLFKDDKYWLISNLRPEPNYPKSIHSFGFPNFVK 378

Qy         142 PLDAAVECHRGECQAEGVLFFQGHGHRNGTGHGNSTHHGPEYMRCSPHLVLSALTSDNHG 201
                :||||                                 | : |
Db         379 KIDAAV-------------------------------FNPRFYR---------------- 391

Qy         202 ATYAFSGTHYWRLDTSRD----GWHSWPIAHQWPQGPSAVDAAFSWEEK-LYLVQGTQVY 256
                || |    ||| |  |     |:      :    ||  :|| |  : |  |  ||:  :
Db         392 -TYFFVDNQYWRYDERRQMMDPGYPKLITKNFQGIGPK-IDAVFYSKNKYYYFFQGSNQF 449

Qy         257 VF 258
                :
Db         450 EY 451

RESULT 12
US-10-131-985-39
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```
; Sequence 39, Application US/10131985
; Publication No. US20030199440A1
; GENERAL INFORMATION:
;  APPLICANT: Dack, Kevin N
;  APPLICANT:  Davies, Michael J
;  APPLICANT:  Fish, Paul V
;  APPLICANT:  Huggins, Jonathan P
;  APPLICANT:  McIntosh, Fraser S
;  APPLICANT:  Occleston, Nicholas L
;  TITLE OF INVENTION: Composition
;  FILE REFERENCE: PCS 10391A
;  CURRENT APPLICATION NUMBER: US/10/131,985
;  CURRENT FILING DATE:  2002-04-25
;  PRIOR APPLICATION NUMBER: US/09/726,295
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: GB 9930768.8
;  PRIOR FILING DATE: 1999-12-29
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-131-985-39

  Query Match             9.3%;  Score 202.5;  DB 14;  Length 470;
  Best Local Similarity   27.3%;  Pred. No. 1.9e-10;
  Matches   66;  Conservative   23;  Mismatches   90;  Indels   63;  Gaps   10;

Qy         30 SAHGNVAEGETKPDPDVTE--RCSDGWSFDATTLDDNGTMLFFKGEFVW----KSHKWDR 83
              | :|:  | :  |:|| :|   |    |||| |   |  : |||  | |    :  |
Db        260 SLYGDPKENQRLPNPDNSEPALCDPNLSFDAVTTVGN-KIFFFKDRFFWLKVSERPKTSV 318

Qy         84 ELISERWKNFPSPVDAAFR-QGHNSVFLIKGDKVWVYPPEKKEKGYPKLLQD-EFPGIPS 141
               |||  |   || ::||:  :  | ||| | || |:    : |  ||| :    ||
Db        319 NLISSLWPTLPSGIEAAYEIEARNQVFLFKDDKYWLISNLRPEPNYPKSIHSFGFPNFVK 378

Qy        142 PLDAAVECHRGECQAEGVLFFQGHGHRNGTGHGNSTHHGPEYMRCSPHLVLSALTSDNHG 201
               :||||                                 | : |
Db        379 KIDAAV-------------------------------FNPRFYR---------------- 391

Qy        202 ATYAFSGTHYWRLDTSRD----GWHSWPIAHQWPQGPSAVDAAFSWEEK-LYLVQGTQVY 256
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RESULT 13
US-10-295-027-324
; Sequence 324, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Aziz, Natasha
;  APPLICANT:  Ginsberg, Wendy M.
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Glynne, Richard
;  APPLICANT:  Hevezi, Peter A.
;  APPLICANT:  Mack, David H.
;  APPLICANT:  Murray, Richard
;  APPLICANT:  Watson, Susan R.
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
;  TITLE OF INVENTION:  Methods of Screening for Modulators of Cancer
;  FILE REFERENCE: 018501-012500US
;  CURRENT APPLICATION NUMBER: US/10/295,027
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: US 09/663,733
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/350,666
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;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/335,394
;  PRIOR FILING DATE: 2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/332,464
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: US 60/334,393
;  PRIOR FILING DATE: 2001-11-29
;  PRIOR APPLICATION NUMBER: US 60/340,376
;  PRIOR FILING DATE: 2001-12-14
;  PRIOR APPLICATION NUMBER: US 60/347,211
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: US 60/347,349
;  PRIOR FILING DATE: 2002-01-10
;  PRIOR APPLICATION NUMBER: US 60/355,250
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/356,714
;  PRIOR FILING DATE: 2002-02-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1386
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 324
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-295-027-324

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  Best Local Similarity   27.3%;  Pred. No. 1.9e-10;
  Matches   66;  Conservative   23;  Mismatches   90;  Indels   63;  Gaps   10;

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Qy        142 PLDAAVECHRGECQAEGVLFFQGHGHRNGTGHGNSTHHGPEYMRCSPHLVLSALTSDNHG 201
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Db        379 KIDAAV-------------------------------FNPRFYR---------------- 391

Qy        202 ATYAFSGTHYWRLDTSRD----GWHSWPIAHQWPQGPSAVDAAFSWEEK-LYLVQGTQVY 256
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Qy        257 VF 258
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Db        450 EY 451

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US-10-295-027-1243
; Sequence 1243, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Aziz, Natasha
;  APPLICANT:  Ginsberg, Wendy M.
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Glynne, Richard
;  APPLICANT:  Hevezi, Peter A.
;  APPLICANT:  Mack, David H.
;  APPLICANT:  Murray, Richard
;  APPLICANT:  Watson, Susan R.
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
;  TITLE OF INVENTION:  Methods of Screening for Modulators of Cancer
;  FILE REFERENCE: 018501-012500US
;  CURRENT APPLICATION NUMBER: US/10/295,027
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: US 09/663,733
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/335,394
;  PRIOR FILING DATE: 2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/332,464
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: US 60/334,393
;  PRIOR FILING DATE: 2001-11-29
;  PRIOR APPLICATION NUMBER: US 60/340,376
;  PRIOR FILING DATE: 2001-12-14
;  PRIOR APPLICATION NUMBER: US 60/347,211
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: US 60/347,349
;  PRIOR FILING DATE: 2002-01-10
;  PRIOR APPLICATION NUMBER: US 60/355,250
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/356,714
;  PRIOR FILING DATE: 2002-02-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1386
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1243
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-295-027-1243

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  Best Local Similarity   27.3%;  Pred. No. 1.9e-10;
  Matches   66;  Conservative   23;  Mismatches   90;  Indels   63;  Gaps   10;

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Db        260 SLYGDPKENQRLPNPDNSEPALCDPNLSFDAVTTVGN-KIFFFKDRFFWLKVSERPKTSV 318

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Db        379 KIDAAV-------------------------------FNPRFYR---------------- 391

Qy        202 ATYAFSGTHYWRLDTSRD----GWHSWPIAHQWPQGPSAVDAAFSWEEK-LYLVQGTQVY 256
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Qy        257 VF 258
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Db        450 EY 451

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; Sequence 1244, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Aziz, Natasha
;  APPLICANT:  Ginsberg, Wendy M.
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Glynne, Richard
;  APPLICANT:  Hevezi, Peter A.
;  APPLICANT:  Mack, David H.
;  APPLICANT:  Murray, Richard
;  APPLICANT:  Watson, Susan R.
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
;  TITLE OF INVENTION:  Methods of Screening for Modulators of Cancer
;  FILE REFERENCE: 018501-012500US
;  CURRENT APPLICATION NUMBER: US/10/295,027
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: US 09/663,733
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/335,394
;  PRIOR FILING DATE: 2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/332,464
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: US 60/334,393
;  PRIOR FILING DATE: 2001-11-29
;  PRIOR APPLICATION NUMBER: US 60/340,376
;  PRIOR FILING DATE: 2001-12-14
;  PRIOR APPLICATION NUMBER: US 60/347,211
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: US 60/347,349
;  PRIOR FILING DATE: 2002-01-10
;  PRIOR APPLICATION NUMBER: US 60/355,250
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/356,714
;  PRIOR FILING DATE: 2002-02-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1386
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1244
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-295-027-1244

  Query Match             9.3%;  Score 202.5;  DB 15;  Length 470;
  Best Local Similarity   27.3%;  Pred. No. 1.9e-10;
  Matches   66;  Conservative   23;  Mismatches   90;  Indels   63;  Gaps   10;

Qy         30 SAHGNVAEGETKPDPDVTE--RCSDGWSFDATTLDDNGTMLFFKGEFVW----KSHKWDR 83
              | :|:  | :  |:|| :|   |    |||| |   |  : |||  | |    :  |
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Qy        202 ATYAFSGTHYWRLDTSRD----GWHSWPIAHQWPQGPSAVDAAFSWEEK-LYLVQGTQVY 256
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Db        392 -TYFFVDNQYWRYDERRQMMDPGYPKLITKNFQGIGPK-IDAVFYSKNKYYYFFQGSNQF 449

Qy        257 VF 258
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Db        450 EY 451

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           Copyright (c) 1993 - 2004  Compugen Ltd.

OM protein - protein search, using sw model

Run on:         June  7, 2004, 08:55:29 ; Search time 22 Seconds
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Perfect score:  2185
Sequence:       1 MARVLGAPVALGLWSLCWSL..........NAAKALPQPQNVTSLLGCTH 391

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Searched:       389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:      389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                  %
Result          Query
  No.   Score   Match Length DB ID                          Description
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    2   202.5    9.3    470  3  US-08-396-988-2              Sequence 2, Appli
    3   202.5    9.3    470  4  US-09-391-104-26             Sequence 26, Appl
    4     199    9.1    517  4  US-09-391-104-32             Sequence 32, Appl
    5     199    9.1    519  3  US-09-211-704A-7             Sequence 7, Appli
    6   189.5    8.7    476  3  US-08-704-711A-21            Sequence 21, Appl
    7   189.5    8.7    476  3  US-08-448-489-14             Sequence 14, Appl
    8   189.5    8.7    476  4  US-09-521-220-21             Sequence 21, Appl
    9   189.5    8.7    476  4  US-09-391-104-22             Sequence 22, Appl
   10   183.5    8.4    444  1  US-09-178-002-2              Sequence 2, Appli
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   20   179.5    8.2    488  4  US-09-521-220-22             Sequence 22, Appl
   21   179.5    8.2    488  4  US-09-391-104-31             Sequence 31, Appl
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   33     176    8.1    471  4  US-08-994-689C-21            Sequence 21, Appl
   34     175    8.0    466  3  US-08-704-711A-17            Sequence 17, Appl
   35     175    8.0    466  4  US-09-521-220-17             Sequence 17, Appl
   36     172    7.9    564  3  US-09-211-704A-8             Sequence 8, Appli
   37     172    7.9    669  3  US-08-704-711A-3             Sequence 3, Appli
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   39     172    7.9    669  4  US-09-391-104-29             Sequence 29, Appl
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   41   167.5    7.7    411  4  US-09-171-545-3              Sequence 3, Appli
   42   167.5    7.7    416  4  US-09-171-545-4              Sequence 4, Appli
   43   167.5    7.7    508  4  US-09-171-545-1              Sequence 1, Appli
   44   164.5    7.5    324  2  US-08-816-755-2              Sequence 2, Appli
   45   164.5    7.5    324  3  US-09-090-673-2              Sequence 2, Appli

                              ALIGNMENTS


RESULT 1
US-08-068-392-2
; Sequence 2, Application US/08068392
; Patent No. 6150152
;  GENERAL INFORMATION:
;    APPLICANT:  Shapiro, Steven M.
;    TITLE OF INVENTION:  Human Macrophage Metalloproteinase
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scott J. Meyer, Monsanto Co., A3SM
;      STREET:  800 N. Lindbergh Blvd.
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63167
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/068,392
;      FILING DATE:  19930528
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyer, Scott J.
;      REGISTRATION NUMBER:  25275
;      REFERENCE/DOCKET NUMBER:  07-24(12406)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)694-3117
;      TELEFAX:  (314)694-5435
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  470 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-068-392-2

  Query Match             9.3%;  Score 202.5;  DB 3;  Length 470;
  Best Local Similarity   27.3%;  Pred. No. 2.9e-12;
  Matches   66;  Conservative   23;  Mismatches   90;  Indels   63;  Gaps   10;

Qy         30 SAHGNVAEGETKPDPDVTE--RCSDGWSFDATTLDDNGTMLFFKGEFVW----KSHKWDR 83
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Qy         202 ATYAFSGTHYWRLDTSRD----GWHSWPIAHQWPQGPSAVDAAFSWEEK-LYLVQGTQVY 256
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Qy         257 VF 258
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Db         450 EY 451


RESULT 2
US-08-396-988-2
; Sequence 2, Application US/08396988
; Patent No. 6204043
;  GENERAL INFORMATION:
;    APPLICANT:  Shapiro, Steven M.
;    TITLE OF INVENTION:  Human Macrophage Metalloproteinase
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scott J. Meyer, Monsanto Co., A3SM
;      STREET:  800 N. Lindbergh Blvd.
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63167
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/396,988
;      FILING DATE:  01-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/068,392
;      FILING DATE:  28-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyer, Scott J.
;      REGISTRATION NUMBER:  25275
;      REFERENCE/DOCKET NUMBER:  07-24(12406)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)694-3117
;      TELEFAX:  (314)694-5435
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  470 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-396-988-2

  Query Match              9.3%;  Score 202.5;  DB 3;  Length 470;
  Best Local Similarity   27.3%;  Pred. No. 2.9e-12;
  Matches   66;  Conservative   23;  Mismatches   90;  Indels   63;  Gaps   10;

Qy          30 SAHGNVAEGETKPDPDVTE--RCSDGWSFDATTLDDNGTMLFFKGEFVW----KSHKWDR 83
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Qy         202 ATYAFSGTHYWRLDTSRD----GWHSWPIAHQWPQGPSAVDAAFSWEEK-LYLVQGTQVY 256
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Db         392 -TYFFVDNQYWRYDERRQMMDPGYPKLITKNFQGIGPK-IDAVFYSKNKYYYFFQGSNQF 449

Qy         257 VF 258
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Db         450 EY 451

RESULT 3
US-09-391-104-26
; Sequence 26, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
;  APPLICANT:  Abbott Laboratories
;  APPLICANT:  Falduto, Michael T.
;  APPLICANT:  Magnuson, Scott R.
;  APPLICANT:  Morgan, Douglas W.
;  TITLE OF INVENTION:  HUMAN MATRIX METALLOPROTEASE GENE,
;  TITLE OF INVENTION:  PROTEINS ENCODED THEREFROM AND METHODS
;  TITLE OF INVENTION:  OF USING SAME
;  FILE REFERENCE:  6073.US.P1
;  CURRENT APPLICATION NUMBER: US/09/391,104
;  CURRENT FILING DATE:  1999-09-07
;  PRIOR APPLICATION NUMBER:  US 08/814,394
;  PRIOR FILING DATE:  1997-03-11
;  NUMBER OF SEQ ID NOS:  35
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 26
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-391-104-26

  Query Match              9.3%;  Score 202.5;  DB 4;  Length 470;
  Best Local Similarity   27.3%;  Pred. No. 2.9e-12;
  Matches   66;  Conservative   23;  Mismatches   90;  Indels   63;  Gaps   10;

Qy          30 SAHGNVAEGETKPDPDVTE--RCSDGWSFDATTLDDNGTMLFFKGEFVW----KSHKWDR 83
               | :|:  | :  |:|| :|   |    |||| |   |  : |||  | |    :  |
Db         260 SLYGDPKENQRLPNPDNSEPALCDPNLSFDAVTTVGN-KIFFFKDRFFWLKVSERPKTSV 318

Qy          84 ELISERWKNFPSPVDAAFR-QGHNSVFLIKGDKVWVYPPEKKEKGYPKLLQD-EFPGIPS 141
                |||  |   || ::||:  :  | ||| | || |:    : |  ||| :    ||
Db         319 NLISSLWPTLPSGIEAAYEIEARNQVFLFKDDKYWLISNLRPEPNYPKSIHSFGFPNFVK 378

Qy         142 PLDAAVECHRGECQAEGVLFFQGHGHRNGTGHGNSTHHGPEYMRCSPHLVLSALTSDNHG 201
                :||||                                 | : |
Db         379 KIDAAV-------------------------------FNPRFYR---------------- 391

Qy         202 ATYAFSGTHYWRLDTSRD----GWHSWPIAHQWPQGPSAVDAAFSWEEK-LYLVQGTQVY 256
                || |    ||| |  |     |:      :    ||  :|| |  : |  |  ||:  :
Db         392 -TYFFVDNQYWRYDERRQMMDPGYPKLITKNFQGIGPK-IDAVFYSKNKYYYFFQGSNQF 449

Qy         257 VF 258
                :
Db         450 EY 451

RESULT 4
US-09-391-104-32
; Sequence 32, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
;  APPLICANT:  Abbott Laboratories
;  APPLICANT:  Falduto, Michael T.
;  APPLICANT:  Magnuson, Scott R.
;  APPLICANT:  Morgan, Douglas W.
;  TITLE OF INVENTION:  HUMAN MATRIX METALLOPROTEASE GENE,
;  TITLE OF INVENTION:  PROTEINS ENCODED THEREFROM AND METHODS
;  TITLE OF INVENTION:  OF USING SAME
;  FILE REFERENCE:  6073.US.P1
;  CURRENT APPLICATION NUMBER: US/09/391,104
;  CURRENT FILING DATE:  1999-09-07
;  PRIOR APPLICATION NUMBER:  US 08/814,394
;  PRIOR FILING DATE:  1997-03-11
;  NUMBER OF SEQ ID NOS:  35
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 32
;   LENGTH: 517
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-391-104-32

  Query Match             9.1%;  Score 199;  DB 4;  Length 517;
  Best Local Similarity   25.0%;  Pred. No. 7.7e-12;
  Matches   80;  Conservative   31;  Mismatches  123;  Indels   86;  Gaps   16;

Qy          5 LGAPVALGL--------WSLCWSLAIATPL-----PPTSAHGNVAEGETKPDPDVTERCS 51
              :| |:  ||        | |       :|      ||             |  ||  |||
Db        188 VGDPLRYGLPYEDKVRVWQLYGVRESVSPTAQPEEPPLLPEPPDNRSSAPPRKDVPHRCS 247

Qy         52 DGWSFDATTLDDNGTMLFFKGEFVWKSHKWDRELISER-------WKNFP---SPVDAAF 101
                  |||      |   ||||:: |:  : || |:| :       |:  |     ||| :
Db        248 T--HFDAVA-QIRGEAFFFKGKYFWRLTR-DRHLVSLQPAQMHRFWRGLPLHLDSVDAVY 303

Qy        102 -RQGHNSVFLIKGDKVWVYPPEKKEKGYPKLLQDEFPGIPSPLDAAVECHRGECQAEGVL 160
               |   : :   |||: ||:     |:|||: : | |   |  :|||
Db        304 ERTSDHKIVFFKGDRYWVFKDNNVEEGYPRPVSD-FSLPPGGIDAA-------------- 348

Qy        161 FFQGHGHRNGTGHGNSTHHGPEYMRCSPHLVLSALTSDNHGATYAFSGTHYWRLDT-SRD 219
              |   |  |                                  || |    ||| |  :|
Db        349 FSWAHNDR----------------------------------TYFFKDQLYWRYDDHTRH 374

Qy        220 GWHSWPI-AHQWPQGPSAVDAAFSWEE-KLYLVQGTQVYVFLTKGGYTLVSGYPKRLEKE 277
                  :|  :  |   || :| |  | :   |  :| | |  :  |   :  |||:   ::
Db        375 MDPGYPAQSPLWRGVPSTLDDAMRWSDGASYFFRG-QEYWKVLDGELEVAPGYPQSTARD 433

Qy        278 -----VGTPHGIILDSVDAA 292
                        | :   ||||
Db        434 WLVCGDSQADGSVAAGVDAA 453


RESULT 5
US-09-211-704A-7
; Sequence 7, Application US/09211704A
; Patent No. 6271014
;  GENERAL INFORMATION:
;    APPLICANT:  de Saint-Vis, Blandine Marie
;    APPLICANT:  Fossiez, Francois
;    APPLICANT:  Caux, Christophe
;    APPLICANT:  Lebecque, Serge J.E.
;    TITLE OF INVENTION:  Mammalian Proteinases; Related Reagents
;    TITLE OF INVENTION:  and Methods
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/211,704A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/005,263
;      FILING DATE:  09-JAN-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
```

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;      REFERENCE/DOCKET NUMBER:  SF0781K
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)852-9196
;      TELEFAX:  (650)496-1200
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  519 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-211-704A-7

  Query Match             9.1%;  Score 199;  DB 3;  Length 519;
  Best Local Similarity   25.0%;  Pred. No. 7.7e-12;
  Matches   80;  Conservative   31;  Mismatches  123;  Indels   86;  Gaps   16;

Qy          5 LGAPVALGL--------WSLCWSLAIATPL-----PPTSAHGNVAEGETKPDPDVTERCS 51
              :| |:  ||        | |       :|      ||             |  ||  |||
Db        190 VGDPLRYGLPYEDKVRVWQLYGVRESVSPTAQPEEPPLLPEPPDNRSSAPPRKDVPHRCS 249

Qy         52 DGWSFDATTLDDNGTMLFFKGEFVWKSHKWDRELISER-------WKNFP---SPVDAAF 101
                  |||      |   ||||:: |:  : || |:| :       |:  |     ||| :
Db        250 T--HFDAVA-QIRGEAFFFKGKYFWRLTR-DRHLVSLQPAQMHRFWRGLPLHLDSVDAVY 305

Qy        102 -RQGHNSVFLIKGDKVWVYPPEKKEKGYPKLLQDEFPGIPSPLDAAVECHRGECQAEGVL 160
               |   : :   |||: ||:     |:|||: : | |   |  :|||
Db        306 ERTSDHKIVFFKGDRYWVFKDNNVEEGYPRPVSD-FSLPPGGIDAA-------------- 350

Qy        161 FFQGHGHRNGTGHGNSTHHGPEYMRCSPHLVLSALTSDNHGATYAFSGTHYWRLDT-SRD 219
              |   |  |                                  || |    ||| |  :|
Db        351 FSWAHNDR----------------------------------TYFFKDQLYWRYDDHTRH 376

Qy        220 GWHSWPI-AHQWPQGPSAVDAAFSWEE-KLYLVQGTQVYVFLTKGGYTLVSGYPKRLEKE 277
                  :|  :  |   || :| |  | :   |  :| | |  :  |   :  |||:   ::
Db        377 MDPGYPAQSPLWRGVPSTLDDAMRWSDGASYFFRG-QEYWKVLDGELEVAPGYPQSTARD 435

Qy        278 -----VGTPHGIILDSVDAA 292
                        | :   ||||
Db        436 WLVCGDSQADGSVAAGVDAA 455


RESULT 6
US-08-704-711A-21
; Sequence 21, Application US/08704711A
; Patent No. 6114159
;  GENERAL INFORMATION:
;    APPLICANT:  WILL, Horst
;    APPLICANT:  HINZMANN, Bernd
;    TITLE OF INVENTION:  DNA SEQUENCES FOR MATRIX
;    TITLE OF INVENTION:  METALLOPROTEASES, THEIR PRODUCTION AND USE
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/704,711A
;      FILING DATE:  20-NOV-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/DE95/00357
;      FILING DATE:  17-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE 4438838.1
;      FILING DATE:  21-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE 4409663.1
;      FILING DATE:  17-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GRANADOS, Patricia D.
;      REGISTRATION NUMBER:  33,683
;      REFERENCE/DOCKET NUMBER:  26083/124
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  476 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-704-711A-21

  Query Match              8.7%;  Score 189.5;  DB 3;  Length 476;
  Best Local Similarity   28.4%;  Pred. No. 6.6e-11;
  Matches   55;  Conservative   24;  Mismatches   42;  Indels   73;  Gaps   10;

Qy          25 PLPPTSAHGNVAEGETKPDPDVTERCSDGWSFDA-TTLDDNGTMLFFKGEFVWKSHKWDR 83
               || ||    :|  |   |      :|    |||| :||   |  ||||  : |:   |:
Db         272 PLVPTK---SVPSGSEMP-----AKCDPALSFDAISTL--RGEYLFFKDRYFWRRSHWNP 321

Qy          84 E----LISERWKNFPSPVDAAFR-QGHNSVFLIKGDKVWV------------------YP 120
               |    |||  | : || :|||:     ::||: ||:: |                   :|
Db         322 EPEFHLISAFWPSLPSYLDAAYEVNSRDTVFIFKGNEFWAIRGNEVQAGYPRGIHTLGFP 381

Qy         121 P------------EKK--------------------EKGYPKLLQDEFPGIPSPLDAAVE 148
               |            |||                    |:|:|:|: |:|||:   :|| :
Db         382 PTIRKIDAAVSDKEKKKTYFFAADKYWRFDENSQSMEQGFPRLIADDFPGVEPKVDAVL- 440

Qy         149 CHRGECQAEGVLFF 162
                     || |  :|
Db         441 ------QAFGFFYF 448

RESULT 7
US-08-448-489-14
; Sequence 14, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
;  APPLICANT: SEIKI, Motoharu
;  APPLICANT: SATO, Hiroshi
;  APPLICANT: SHINAGAWA, Akira
;  TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
;  FILE REFERENCE: 55-290P
;  CURRENT APPLICATION NUMBER: US/08/448,489
;  CURRENT FILING DATE: 1995-06-07
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 476
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: Known Member of
;   OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-14

  Query Match              8.7%;  Score 189.5;  DB 3;  Length 476;
  Best Local Similarity   28.4%;  Pred. No. 6.6e-11;
  Matches   55;  Conservative   24;  Mismatches   42;  Indels   73;  Gaps   10;

Qy          25 PLPPTSAHGNVAEGETKPDPDVTERCSDGWSFDA-TTLDDNGTMLFFKGEFVWKSHKWDR 83
               || ||    :|  |   |      :|    |||| :||   |  ||||  : |:   |:
Db         272 PLVPTK---SVPSGSEMP-----AKCDPALSFDAISTL--RGEYLFFKDRYFWRRSHWNP 321

Qy          84 E----LISERWKNFPSPVDAAFR-QGHNSVFLIKGDKVWV------------------YP 120
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               |    |||  | : || :|||:     ::||: ||:: |                   :|
Db         322 EPEFHLISAFWPSLPSYLDAAYEVNSRDTVFIFKGNEFWAIRGNEVQAGYPRGIHTLGFP 381

Qy         121 P------------EKK--------------------EKGYPKLLQDEFPGIPSPLDAAVE 148
               |            |||                    |:|:|:|: |:|||:   :|| :
Db         382 PTIRKIDAAVSDKEKKKTYFFAADKYWRFDENSQSMEQGFPRLIADDFPGVEPKVDAVL- 440

Qy         149 CHRGECQAEGVLFF 162
                     || |  :|
Db         441 ------QAFGFFYF 448

RESULT 8
US-09-521-220-21
; Sequence 21, Application US/09521220
; Patent No. 6399348
;  GENERAL INFORMATION:
;       APPLICANT: WILL, Horst
;                  HINZMANN, Bernd
;       TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
;                           METALLOPROTEASSES, THEIR PRODUCTION AND USE
;       NUMBER OF SEQUENCES: 22
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/521,220
;            FILING DATE: 08-Mar-2000
;            CLASSIFICATION: <Unknown>
;                            21-OCT-1994
;                            17-MAR-1994
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/704,711
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: DE 4438838.1
;            FILING DATE: 21-OCT-1994
;            APPLICATION NUMBER: DE 4409663.1
;            FILING DATE: 17-MAR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: GRANADOS, Patricia D.
;            REGISTRATION NUMBER: 33,683
;            REFERENCE/DOCKET NUMBER: 26083/124
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 21:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 476 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-521-220-21

  Query Match              8.7%;  Score 189.5;  DB 4;  Length 476;
  Best Local Similarity   28.4%;  Pred. No. 6.6e-11;
  Matches   55;  Conservative   24;  Mismatches   42;  Indels   73;  Gaps   10;

Qy          25 PLPPTSAHGNVAEGETKPDPDVTERCSDGWSFDA-TTLDDNGTMLFFKGEFVWKSHKWDR 83
               || ||    :|  |   |      :|    |||| :||   |  ||||  : |:   |:
Db         272 PLVPTK---SVPSGSEMP-----AKCDPALSFDAISTL--RGEYLFFKDRYFWRRSHWNP 321

Qy          84 E----LISERWKNFPSPVDAAFR-QGHNSVFLIKGDKVWV------------------YP 120
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                |    |||  | : || :|||:     ::||: ||:: |                   :|
Db          322 EPEFHLISAFWPSLPSYLDAAYEVNSRDTVFIFKGNEFWAIRGNEVQAGYPRGIHTLGFP 381

Qy          121 P------------EKK--------------------EKGYPKLLQDEFPGIPSPLDAAVE 148
                |            |||                    |:|:|:|: |:|||:   :|| :
Db          382 PTIRKIDAAVSDKEKKKTYFFAADKYWRFDENSQSMEQGFPRLIADDFPGVEPKVDAVL- 440

Qy          149 CHRGECQAEGVLFF 162
                      || |  :|
Db          441 ------QAFGFFYF 448

RESULT 9
US-09-391-104-22
; Sequence 22, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
;  APPLICANT:  Abbott Laboratories
;  APPLICANT:  Falduto, Michael T.
;  APPLICANT:  Magnuson, Scott R.
;  APPLICANT:  Morgan, Douglas W.
;  TITLE OF INVENTION:  HUMAN MATRIX METALLOPROTEASE GENE,
;  TITLE OF INVENTION:  PROTEINS ENCODED THEREFROM AND METHODS
;  TITLE OF INVENTION:  OF USING SAME
;  FILE REFERENCE:  6073.US.P1
;  CURRENT APPLICATION NUMBER: US/09/391,104
;  CURRENT FILING DATE:  1999-09-07
;  PRIOR APPLICATION NUMBER:  US 08/814,394
;  PRIOR FILING DATE:  1997-03-11
;  NUMBER OF SEQ ID NOS:  35
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 22
;   LENGTH: 476
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-391-104-22

  Query Match             8.7%;  Score 189.5;  DB 4;  Length 476;
  Best Local Similarity   28.4%;  Pred. No. 6.6e-11;
  Matches   55;  Conservative   24;  Mismatches   42;  Indels   73;  Gaps   10;

Qy           25 PLPPTSAHGNVAEGETKPDPDVTERCSDGWSFDA-TTLDDNGTMLFFKGEFVWKSHKWDR 83
                || ||    :|  |   |      :|    |||| :||   |  ||||  : |:   |:
Db          272 PLVPTK---SVPSGSEMP-----AKCDPALSFDAISTL--RGEYLFFKDRYFWRRSHWNP 321

Qy           84 E----LISERWKNFPSPVDAAFR-QGHNSVFLIKGDKVWV------------------YP 120
                |    |||  | : || :|||:     ::||: ||:: |                   :|
Db          322 EPEFHLISAFWPSLPSYLDAAYEVNSRDTVFIFKGNEFWAIRGNEVQAGYPRGIHTLGFP 381

Qy          121 P------------EKK--------------------EKGYPKLLQDEFPGIPSPLDAAVE 148
                |            |||                    |:|:|:|: |:|||:   :|| :
Db          382 PTIRKIDAAVSDKEKKKTYFFAADKYWRFDENSQSMEQGFPRLIADDFPGVEPKVDAVL- 440

Qy          149 CHRGECQAEGVLFF 162
                      || |  :|
Db          441 ------QAFGFFYF 448

RESULT 10
US-09-178-002-2
; Sequence 2, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
;  APPLICANT: Hu, Shou-Ih
;  TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
;  FILE REFERENCE: CGC 2048
;  CURRENT APPLICATION NUMBER: US/09/178,002
;  CURRENT FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 444
;   TYPE: PRT
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;   ORGANISM: Homo sapiens
US-09-178-002-2

  Query Match             8.4%;  Score 183.5;  DB 1;  Length 444;
  Best Local Similarity   24.4%;  Pred. No. 2.5e-10;
  Matches   60;  Conservative   31;  Mismatches   80;  Indels   75;  Gaps   10;

Qy           23 ATPLPPTSAHGNVAEGETKPDPDVTERCSDGWSFDA-TTLDDNGTMLFFKGEFVWKSH-- 79
                : |: ||        | : | |     |    :||| |||   | :||||  : |: |
Db          242 SNPIQPT--------GPSTPKP-----CDPSLTFDAITTL--RGEILFFKDRYFWRRHPQ 286

Qy           80 --KWDRELISERWKNFPSPVDAAFRQ-GHNSVFLIKGDKVWVYPPEKKEKGYPKLLQD-E 135
                  : :   ||  | : |: : ||:     : :|| ||:: |        :|||| : :
Db          287 LQRVEMNFISLFWPSLPTGIQAAYEDFDRDLIFLFKGNQYWALSGYDILQGYPKDISNYG 346

Qy          136 FPGIPSPLDAAVECHRGECQAEGVLFFQGHGHRNGTGHGNSTHHGPEYMRCSPHLVLSAL 195
                ||     :||||             |::
Db          347 FPSSVQAIDAAV-------------FYR-------------------------------- 361

Qy          196 TSDNHGATYAFSGTHYWRLDTSR---DGWHSWPIAHQWPQGPSAVDAAFSWEEKLYLVQG 252
                       || |    :|| |  |   :  :   |:  :|   | ||| |  |    :: |
Db          362 -----SKTYFFVNDQFWRYDNQRQFMEPGYPKSISGAFPGIESKVDAVFQQEHFFHVFSG 416

Qy          253 TQVYVF 258
                 : | |
Db          417 PRYYAF 422

RESULT 11
US-09-178-002-4
; Sequence 4, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
;  APPLICANT: Hu, Shou-Ih
;  TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
;  FILE REFERENCE: CGC 2048
;  CURRENT APPLICATION NUMBER: US/09/178,002
;  CURRENT FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-178-002-4

  Query Match             8.4%;  Score 183.5;  DB 1;  Length 467;
  Best Local Similarity   24.4%;  Pred. No. 2.7e-10;
  Matches   60;  Conservative   31;  Mismatches   80;  Indels   75;  Gaps   10;

Qy           23 ATPLPPTSAHGNVAEGETKPDPDVTERCSDGWSFDA-TTLDDNGTMLFFKGEFVWKSH-- 79
                : |: ||        | : | |     |    :||| |||   | :||||  : |: |
Db          265 SNPIQPT--------GPSTPKP-----CDPSLTFDAITTL--RGEILFFKDRYFWRRHPQ 309

Qy           80 --KWDRELISERWKNFPSPVDAAFRQ-GHNSVFLIKGDKVWVYPPEKKEKGYPKLLQD-E 135
                  : :   ||  | : |: : ||:     : :|| ||:: |        :|||| : :
Db          310 LQRVEMNFISLFWPSLPTGIQAAYEDFDRDLIFLFKGNQYWALSGYDILQGYPKDISNYG 369

Qy          136 FPGIPSPLDAAVECHRGECQAEGVLFFQGHGHRNGTGHGNSTHHGPEYMRCSPHLVLSAL 195
                ||     :||||             |::
Db          370 FPSSVQAIDAAV-------------FYR-------------------------------- 384

Qy          196 TSDNHGATYAFSGTHYWRLDTSR---DGWHSWPIAHQWPQGPSAVDAAFSWEEKLYLVQG 252
                       || |    :|| |  |   :  :   |:  :|   | ||| |  |    :: |
Db          385 -----SKTYFFVNDQFWRYDNQRQFMEPGYPKSISGAFPGIESKVDAVFQQEHFFHVFSG 439

Qy          253 TQVYVF 258
                 : | |
Db          440 PRYYAF 445

RESULT 12
US-09-391-104-24
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; Sequence 24, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
;  APPLICANT:  Abbott Laboratories
;  APPLICANT:  Falduto, Michael T.
;  APPLICANT:  Magnuson, Scott R.
;  APPLICANT:  Morgan, Douglas W.
;  TITLE OF INVENTION:  HUMAN MATRIX METALLOPROTEASE GENE,
;  TITLE OF INVENTION:  PROTEINS ENCODED THEREFROM AND METHODS
;  TITLE OF INVENTION:  OF USING SAME
;  FILE REFERENCE:  6073.US.P1
;  CURRENT APPLICATION NUMBER: US/09/391,104
;  CURRENT FILING DATE:  1999-09-07
;  PRIOR APPLICATION NUMBER:  US 08/814,394
;  PRIOR FILING DATE:  1997-03-11
;  NUMBER OF SEQ ID NOS:  35
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 24
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-391-104-24

  Query Match              8.4%;  Score 183.5;  DB 4;  Length 467;
  Best Local Similarity   24.4%;  Pred. No. 2.7e-10;
  Matches   60;  Conservative   31;  Mismatches   80;  Indels   75;  Gaps   10;

Qy          23 ATPLPPTSAHGNVAEGETKPDPDVTERCSDGWSFDA-TTLDDNGTMLFFKGEFVWKSH-- 79
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Db         265 SNPIQPT--------GPSTPKP-----CDPSLTFDAITTL--RGEILFFKDRYFWRRHPQ 309

Qy          80 --KWDRELISERWKNFPSPVDAAFRQ-GHNSVFLIKGDKVWVYPPEKKEKGYPKLLQD-E 135
                 : :   ||  | : |: : ||:     : :|| ||:: |        :|||| : :
Db         310 LQRVEMNFISLFWPSLPTGIQAAYEDFDRDLIFLFKGNQYWALSGYDILQGYPKDISNYG 369

Qy         136 FPGIPSPLDAAVECHRGECQAEGVLFFQGHGHRNGTGHGNSTHHGPEYMRCSPHLVLSAL 195
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Db         370 FPSSVQAIDAAV-------------FYR-------------------------------- 384

Qy         196 TSDNHGATYAFSGTHYWRLDTSR---DGWHSWPIAHQWPQGPSAVDAAFSWEEKLYLVQG 252
                      || |    :|| |  |   :  :   |:  :|   | ||| |  |   ::  |
Db         385 -----SKTYFFVNDQFWRYDNQRQFMEPGYPKSISGAFPGIESKVDAVFQQEHFFHVFSG 439

Qy         253 TQVYVF 258
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Db         440 PRYYAF 445

RESULT 13
US-08-448-489-13
; Sequence 13, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
;  APPLICANT: SEIKI, Motoharu
;  APPLICANT: SATO, Hiroshi
;  APPLICANT: SHINAGAWA, Akira
;  TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
;  FILE REFERENCE: 55-290P
;  CURRENT APPLICATION NUMBER: US/08/448,489
;  CURRENT FILING DATE: 1995-06-07
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 468
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: X = UNKNOWN
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: Known Member of
;   OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-13

  Query Match              8.4%;  Score 183.5;  DB 3;  Length 468;
  Best Local Similarity   24.4%;  Pred. No. 2.7e-10;
  Matches   60;  Conservative   31;  Mismatches   80;  Indels   75;  Gaps   10;

Qy          23 ATPLPPTSAHGNVAEGETKPDPDVTERCSDGWSFDA-TTLDDNGTMLFFKGEFVWKSH-- 79
               : |: ||        | : | |     |    :||| |||   | :||||  : |: |
Db         265 SNPIQPT--------GPSTPKP-----CDPSLTFDAITTL--RGEILFFKDRYFWRRHPQ 309

Qy          80 --KWDRELISERWKNFPSPVDAAFRQ-GHNSVFLIKGDKVWVYPPEKKEKGYPKLLQD-E 135
                 : :   ||  | : |: : ||:     : :|| ||:: |        :|||| : :
Db         310 LQRVEMNFISLFWPSLPTGIQAAYEDFDRDLIFLFKGNQYWALSGYDILQGYPKDISNYG 369

Qy         136 FPGIPSPLDAAVECHRGECQAEGVLFFQGHGHRNGTGHGNSTHHGPEYMRCSPHLVLSAL 195
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Qy         196 TSDNHGATYAFSGTHYWRLDTSR---DGWHSWPIAHQWPQGPSAVDAAFSWEEKLYLVQG 252
                      || |    :|| |  |   :  :   |:  :|   | ||| |  |   ::  |
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RESULT 14
US-09-391-104-23
; Sequence 23, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
;  APPLICANT:  Abbott Laboratories
;  APPLICANT:  Falduto, Michael T.
;  APPLICANT:  Magnuson, Scott R.
;  APPLICANT:  Morgan, Douglas W.
;  TITLE OF INVENTION:  HUMAN MATRIX METALLOPROTEASE GENE,
;  TITLE OF INVENTION:  PROTEINS ENCODED THEREFROM AND METHODS
;  TITLE OF INVENTION:  OF USING SAME
;  FILE REFERENCE:  6073.US.P1
;  CURRENT APPLICATION NUMBER: US/09/391,104
;  CURRENT FILING DATE:  1999-09-07
;  PRIOR APPLICATION NUMBER:  US 08/814,394
;  PRIOR FILING DATE:  1997-03-11
;  NUMBER OF SEQ ID NOS:  35
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 23
;   LENGTH: 469
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-391-104-23

  Query Match              8.3%;  Score 181.5;  DB 4;  Length 469;
  Best Local Similarity   26.3%;  Pred. No. 4.3e-10;
  Matches   59;  Conservative   26;  Mismatches   82;  Indels   57;  Gaps    8;

Qy          44 PDVTERCSDGWSFDA-TTLDDNGTMLFFKGEFVWKSHKWDREL----ISERWKNFPSPVD 98
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Qy          99 AAFR-QGHNSVFLIKGDKVWVYPPEKKEKGYPKLLQDEFPGIPSPLDAAVECHRGECQAE 157
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Db         330 AAYEFADRDEVRFFKGNKYWAVQGQNVLHGYPKDIYSSF-GFP----------------- 371

Qy         158 GVLFFQGHGHRNGTGHGNSTHHGPEYMRCSPHLVLSALTSDNHGATYAFSGTHYWRLD-- 215
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Db         372 ---------------------------RTVKH-IDAALSEENTGKTYFFVANKYWRYDEY 403

Qy         216 -TSRDGWHSWPIAHQWPQGPSAVDAAFSWEEKLYLVQGTQVYVF 258
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RESULT 15
US-07-794-393-4
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; Sequence 4, Application US/07794393
; Patent No. 5236844
;  GENERAL INFORMATION:
;    APPLICANT:  CHAMBON, PIERRE
;    APPLICANT:  BASSET, PAUL
;    APPLICANT:  BELLOCQ, JEAN-PIERRE
;    TITLE OF INVENTION:  ANALYTICAL MARKERS FOR MALIGNANT BREAST
;    TITLE OF INVENTION:  CANCER
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1225 Connecticut Ave. NW Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/794,393
;      FILING DATE:  19911121
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9025326.1
;      FILING DATE:  21-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GOLDSTEIN, JORGE A
;      REGISTRATION NUMBER:  29,021
;      REFERENCE/DOCKET NUMBER:  1383.0040000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 466-0800
;      TELEFAX:  (202) 833-8716
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  492 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-794-393-4

  Query Match             8.3%;  Score 181.5;  DB 1;  Length 492;
  Best Local Similarity   25.2%;  Pred. No. 4.7e-10;
  Matches   69;  Conservative   26;  Mismatches   86;  Indels   93;  Gaps   13;

Qy         24 TPLPPTSAH-----GNVAEGETKPDPDVTERCSDGWSFDATTLDDNGTMLFFKGEFVWKS 78
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Qy         79 HKWDRE-----LISERWKNFPSPVDAAFRQGHNSVFLIKGDKVWVYPPEKKEKGYPKLLQ 133
                   :     | |  |:  ||||||||      ::  :| : |||  ||   |   | :
Db        324 RSGRLQPGYPALASRHWQGLPSPVDAAFEDAQGQIWFFQGAQYWVYDGEKPVLGPAPLSK 383

Qy        134 DEFPGIPSPLDAAVECHRGECQAEGVLFFQGHGHRNGTGHGNSTHHGPEYMRCSPHLVLS 193
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Db        384 LGLQG--SPVHAALV------------------------------WGPE----------- 400

Qy        194 ALTSDNHGATYAFSGTHYWRLD--TSR-DGWHSWPIAHQ---WPQGPSAVDAAFSWEEKL 247
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Db        401 ------KNKIYFFRGGDYWRFHPRTQRVDN----PVPRRSTDWRGVPSEIDAAF------ 444

Qy        248 YLVQGTQVYVFLTKG---------GYTLVSGYPK 272
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Search completed: June  7, 2004, 09:08:12
Job time : 23 secs
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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2004  Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:          June  8, 2004, 05:38:24 ; Search time 535 Seconds
                                          (without alignments)
                                          3334.094 Million cell updates/sec

Title:           US-09-900-448-2
Perfect score:   2185
Sequence:        1 MARVLGAPVALGLWSLCWSL..........NAAKALPQPQNVTSLLGCTH 391

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                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters:      5991872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US09900448/runat_07062004_094659_20503/app_query.fasta_1.583
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09900448_@CGN_1_1_221_@runat_07062004_094659_20503
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       Published_Applications_NA:*
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                 SUMMARIES

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Result                 Query
   No.    Score  Match Length DB  ID                          Description
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     1     2185  100.0   3186  11  US-09-900-448-1            Sequence 1, Appli
     2   2139.5   97.9   1631  15  US-10-125-237-19           Sequence 19, Appl
     3   2139.5   97.9   1631  15  US-10-105-891-19           Sequence 19, Appl
     4   1556.5   71.2   1516  15  US-10-175-523-84           Sequence 84, Appl
     5   1556.5   71.2   1516  15  US-10-316-253-39           Sequence 39, Appl
     6     1338   61.2    861  16  US-10-162-335-87           Sequence 87, Appl
     7      921   42.2  13737  11  US-09-900-448-3            Sequence 3, Appli
     8      771   35.3    488  10  US-09-918-995-30828        Sequence 30828, A
     9      754   34.5    422  10  US-09-918-995-8595         Sequence 8595, Ap
    10      714   32.7    492  10  US-09-918-995-31395        Sequence 31395, A
    11      709   32.4    488  10  US-09-918-995-30754        Sequence 30754, A
    12      663   30.3    491  10  US-09-918-995-32820        Sequence 32820, A
    13      593   27.1    420  9  US-09-960-352-10323        Sequence 10323, A
    14    552.5   25.3    384  10  US-09-918-995-7738         Sequence 7738, Ap
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    16      536   24.5    408  9  US-09-960-352-7040         Sequence 7040, Ap
    17      518   23.7    374  9  US-09-960-352-5368         Sequence 5368, Ap
    18      513   23.5    437  9  US-09-960-352-380          Sequence 380, App
    19    512.5   23.5    405  9  US-09-960-352-445          Sequence 445, App
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    25    483.5   22.1    412  9  US-09-960-352-2507         Sequence 2507, Ap
    26      483   22.1    387  9  US-09-960-352-11316        Sequence 11316, A
    27    480.5   22.0    412  9  US-09-960-352-8662         Sequence 8662, Ap
    28    479.5   21.9    408  9  US-09-960-352-7025         Sequence 7025, Ap
    29    476.5   21.8    418  9  US-09-960-352-13395        Sequence 13395, A
    30    468.5   21.4    405  9  US-09-960-352-2956         Sequence 2956, Ap
    31    468.5   21.4    407  9  US-09-960-352-6107         Sequence 6107, Ap
    32    464.5   21.3    397  9  US-09-960-352-4643         Sequence 4643, Ap
    33    464.5   21.3    407  9  US-09-960-352-136          Sequence 136, App
    34    461.5   21.1    439  9  US-09-960-352-13402        Sequence 13402, A
    35    458.5   21.0    396  9  US-09-960-352-8898         Sequence 8898, Ap
    36      457   20.9    397  9  US-09-960-352-12936        Sequence 12936, A
    37      457   20.9    404  9  US-09-960-352-7514         Sequence 7514, Ap
    38      456   20.9    396  9  US-09-960-352-4209         Sequence 4209, Ap
    39      456   20.9    411  9  US-09-960-352-5619         Sequence 5619, Ap
    40      454   20.8    399  9  US-09-960-352-457          Sequence 457, App
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    42      451   20.6    384  9  US-09-960-352-9132         Sequence 9132, Ap
    43      451   20.6    407  9  US-09-960-352-5920         Sequence 5920, Ap
    44      447   20.5    431  9  US-09-960-352-7320         Sequence 7320, Ap
    45      444   20.3    407  9  US-09-960-352-13635        Sequence 13635, A


                                 ALIGNMENTS

RESULT 1
US-09-900-448-1
; Sequence 1, Application US/09900448
; Publication No. US20030220488A1
; GENERAL INFORMATION:
;  APPLICANT: CECCARDI, Toni et al.
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001272
;  CURRENT APPLICATION NUMBER: US/09/900,448
;  CURRENT FILING DATE:  2001-07-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 3186
;   TYPE: DNA
;   ORGANISM: Human
US-09-900-448-1

Alignment Scores:
Pred. No.:              1.58e-230     Length:        3186
Score:                  2185.00       Matches:       391
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Best Local Similarity:  100.00%      Mismatches:     0
Query Match:            100.00%      Indels:         0
DB:                     11           Gaps:           0

US-09-900-448-2 (1-391) x US-09-900-448-1 (1-3186)

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Db         15 ATGGCTAGGGTACTGGGAGCACCCGTTGCACTGGGGTTGTGGAGCCTATGCTGGTCTCTG 74

Qy         21 AlaIleAlaThrProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGluThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         75 GCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTGCTGAAGGCGAGACC 134

Qy         41 LysProAspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAlaThrThr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 AAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCTTTGATGCTACCACC 194

Qy         61 LeuAspAspAsnGlyThrMetLeuPhePheLysGlyGluPheValTrpLysSerHisLys 80
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Db        195 CTGGATGACAATGGAACCATGCTGTTTTTTAAAGGGGAGTTTGTGTGGAAGAGTCACAAA 254

Qy         81 TrpAspArgGluLeuIleSerGluArgTrpLysAsnPheProSerProValAspAlaAla 100
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Db        255 TGGGACCGGGAGTTAATCTCAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCA 314

Qy        101 PheArgGlnGlyHisAsnSerValPheLeuIleLysGlyAspLysValTrpValTyrPro 120
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Qy        121 ProGluLysLysGluLysGlyTyrProLysLeuLeuGlnAspGluPheProGlyIlePro 140
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Db        375 CCTGAAAAGAAGGAGAAAGGATACCCAAAGTTGCTCCAAGATGAATTTCCTGGAATCCCA 434

Qy        141 SerProLeuAspAlaAlaValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeu 160
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Qy        161 PhePheGlnGlyHisGlyHisArgAsnGlyThrGlyHisGlyAsnSerThrHisHisGly 180
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Qy        201 GlyAlaThrTyrAlaPheSerGlyThrHisTyrTrpArgLeuAspThrSerArgAspGly 220
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Qy        221 TrpHisSerTrpProIleAlaHisGlnTrpProGlnGlyProSerAlaValAspAlaAla 240
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Qy        241 PheSerTrpGluGluLysLeuTyrLeuValGlnGlyThrGlnValTyrValPheLeuThr 260
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Db        735 TTTTCCTGGGAAGAAAAACTCTATCTGGTCCAGGGCACCCAGGTATATGTCTTCCTGACA 794

Qy        261 LysGlyGlyTyrThrLeuValSerGlyTyrProLysArgLeuGluLysGluValGlyThr 280
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Db        795 AAGGGAGGCTATACCCTAGTAAGCGGTTATCCGAAGCGGCTGGAGAAGGAAGTCGGGACC 854

Qy        281 ProHisGlyIleIleLeuAspSerValAspAlaAlaPheIleCysProGlySerSerArg 300
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Qy        301 LeuHisIleMetAlaGlyArgArgLeuTrpTrpLeuAspLeuLysSerGlyAlaGlnAla 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        915 CTCCATATCATGGCAGGACGGCGGCTGTGGTGGCTGGACCTGAAGTCAGGAGCCCAAGCC 974

Qy        321 ThrTrpThrGluLeuProTrpProHisGluLysValAspGlyAlaLeuCysMetGluLys 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        975 ACGTGGACAGAGCTTCCTTGGCCCCATGAGAAGGTAGACGGAGCCTTGTGTATGGAAAAG 1034

Qy        341 SerLeuGlyProAsnSerCysSerAlaAsnGlyProGlyLeuTyrLeuIleHisGlyPro 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1035 TCCCTTGGCCCTAACTCATGTTCCGCCAATGGTCCCGGCTTGTACCTCATCCATGGTCCC 1094

Qy        361 AsnLeuTyrCysTyrSerAspValGluLysLeuAsnAlaAlaLysAlaLeuProGlnPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1095 AATTTGTACTGCTACAGTGATGTGGAGAAACTGAATGCAGCCAAGGCCCTTCCGCAACCC 1154

Qy        381 GlnAsnValThrSerLeuLeuGlyCysThrHis 391
              |||||||||||||||||||||||||||||||||
Db       1155 CAGAATGTGACCAGTCTCCTGGGCTGCACTCAC 1187

RESULT 2
US-10-125-237-19
; Sequence 19, Application US/10125237
; Publication No. US20030022329A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: No. US20030022329Alel Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 791CIP2ADIV
;  CURRENT APPLICATION NUMBER: US/10/125,237
;  CURRENT FILING DATE:  2002-04-17
;  PRIOR APPLICATION NUMBER: 09/668,317
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: 09/552,929
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 91
;  SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 19
;   LENGTH: 1631
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (71)..(1459)
US-10-125-237-19

Alignment Scores:
Pred. No.:                7.01e-226      Length:         1631
Score:                    2139.50        Matches:        391
Percent Similarity:       84.63%         Conservative:   0
Best Local Similarity:    84.63%         Mismatches:     0
Query Match:              97.92%         Indels:         71
DB:                       15             Gaps:           1

US-09-900-448-2 (1-391) x US-10-125-237-19 (1-1631)

Qy          1 MetAlaArgValLeuGlyAlaProValAlaLeuGlyLeuTrpSerLeuCysTrpSerLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 ATGGCTAGGGTACTGGGAGCACCCGTTGCACTGGGGTTGTGGAGCCTATGCTGGTCTCTG 130

Qy         21 AlaIleAlaThrProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGluThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 GCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTGCTGAAGGCGAGACC 190

Qy         41 LysProAspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAlaThrThr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 AAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCTTTGATGCTACCACC 250

Qy         61 LeuAspAspAsnGlyThrMetLeuPhePheLysGlyGluPheValTrpLysSerHisLys 80
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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     251 CTGGATGACAATGGAACCATGCTGTTTTTAAAGGGGAGTTTGTGTGGAAGAGTCACAAA 310

Qy      81 TrpAspArgGluLeuIleSerGluArgTrpLysAsnPheProSerProValAspAlaAla 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     311 TGGGACCGGGAGTTAATCTCAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCA 370

Qy     101 PheArgGlnGlyHisAsnSerValPheLeuIleLysGlyAspLysValTrpValTyrPro 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     371 TTCCGTCAAGGTCACAACAGTGTCTTTCTGATCAAGGGGGACAAAGTCTGGGTATACCCT 430

Qy     121 ProGluLysLysGluLysGlyTyrProLysLeuLeuGlnAspGluPheProGlyIlePro 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     431 CCTGAAAAGAAGGAGAAAGGATACCCAAAGTTGCTCCAAGATGAATTTCCTGGAATCCCA 490

Qy     141 SerProLeuAspAlaAlaValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeu 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     491 TCCCCACTGGATGCAGCTGTGGAATGTCACCGTGGAGAATGTCAAGCTGAAGGCGTCCTC 550

Qy     161 PhePheGln--------------------------------------------------- 163
           |||||||||
Db     551 TTCTTCCAAGGTGACCGCGAGTGGTTCTGGGACTTGGCTACGGGAACCATGAAGGAGCGT 610

Qy     163 ------------------------------------------------------------ 163

Db     611 TCCTGGCCAGCTGTTGGGAACTGCTCCTCTGCCCTGAGATGGCTGGGCCGCTACTACTGC 670

Qy     163 ------------------------------------------------------------ 163

Db     671 TTCCAGGGTAACCAATTCCTGCGCTTCGACCCTGTCAGGGGAGAGGTGCCTCCCAGGTAC 730

Qy     164 ------------------------------------------GlyHisGlyHisArgAsn 169
                                                     ||||||||||||||||||
Db     731 CCGCGGGATGTCCGAGACTACTTCATGCCCTGCCCTGGCAGAGGCCATGGACACAGGAAT 790

Qy     170 GlyThrGlyHisGlyAsnSerThrHisHisGlyProGluTyrMetArgCysSerProHis 189
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     791 GGGACTGGCCATGGGAACAGTACCCACCATGGCCCTGAGTATATGCGCTGTAGCCCACAT 850

Qy     190 LeuValLeuSerAlaLeuThrSerAspAsnHisGlyAlaThrTyrAlaPheSerGlyThr 209
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     851 CTAGTCTTGTCTGCACTGACGTCTGACAACCATGGTGCCACCTATGCCTTCAGTGGGACC 910

Qy     210 HisTyrTrpArgLeuAspThrSerArgAspGlyTrpHisSerTrpProIleAlaHisGln 229
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     911 CACTACTGGCGTCTGGACACCAGCCGGGATGGCTGGCATAGCTGGCCCATTGCTCATCAG 970

Qy     230 TrpProGlnGlyProSerAlaValAspAlaAlaPheSerTrpGluGluLysLeuTyrLeu 249
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     971 TGGCCCCAGGGTCCTTCAGCAGTGGATGCTGCCTTTTCCTGGGAAGAAAAACTCTATCTG 1030

Qy     250 ValGlnGlyThrGlnValTyrValPheLeuThrLysGlyGlyTyrThrLeuValSerGly 269
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1031 GTCCAGGGCACCCAGGTATATGTCTTCCTGACAAAGGGAGGCTATACCCTAGTAAGCGGT 1090

Qy     270 TyrProLysArgLeuGluLysGluValGlyThrProHisGlyIleIleLeuAspSerVal 289
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1091 TATCCGAAGCGGCTGGAGAAGGAAGTCGGGACCCCTCATGGGATTATCCTGGACTCTGTG 1150

Qy     290 AspAlaAlaPheIleCysProGlySerSerArgLeuHisIleMetAlaGlyArgArgLeu 309
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1151 GATGCGGCCTTTATCTGCCCTGGGTCTTCTCGGCTCCATATCATGGCAGGACGGCGGCTG 1210

Qy     310 TrpTrpLeuAspLeuLysSerGlyAlaGlnAlaThrTrpThrGluLeuProTrpProHis 329
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1211 TGGTGGCTGGACCTGAAGTCAGGAGCCCAAGCCACGTGGACAGAGCTTCCTTGGCCCCAT 1270

Qy     330 GluLysValAspGlyAlaLeuCysMetGluLysSerLeuGlyProAsnSerCysSerAla 349
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1271 GAGAAGGTAGACGGAGCCTTGTGTATGGAAAAGTCCCTTGGCCCTAACTCATGTTCCGCC 1330

Qy     350 AsnGlyProGlyLeuTyrLeuIleHisGlyProAsnLeuTyrCysTyrSerAspValGlu 369
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1331 AATGGTCCCGGCTTGTACCTCATCCATGGTCCCAATTTGTACTGCTACAGTGATGTGGAG 1390

Qy     370 LysLeuAsnAlaAlaLysAlaLeuProGlnProGlnAsnValThrSerLeuLeuGlyCys 389
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1391 AAACTGAATGCAGCCAAGGCCCTTCCGCAACCCCAGAATGTGACCAGTCTCCTGGGCTGC 1450

Qy     390 ThrHis 391
           ||||||
Db    1451 ACTCAC 1456

RESULT 3
US-10-105-891-19
; Sequence 19, Application US/10105891
; Publication No. US20030073099A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: No. US20030073099Alel Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 791CIP2A
;  CURRENT APPLICATION NUMBER: US/10/105,891
;  CURRENT FILING DATE:  2002-03-25
;  PRIOR APPLICATION NUMBER: 09/668,317
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: 09/552,929
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 91
;  SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 19
;   LENGTH: 1631
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (71)..(1459)
US-10-105-891-19

Alignment Scores:
Pred. No.:               7.01e-226      Length:         1631
Score:                   2139.50        Matches:        391
Percent Similarity:      84.63%         Conservative:   0
Best Local Similarity:   84.63%         Mismatches:     0
Query Match:             97.92%         Indels:         71
DB:                      15             Gaps:           1

US-09-900-448-2 (1-391) x US-10-105-891-19 (1-1631)

Qy       1 MetAlaArgValLeuGlyAlaProValAlaLeuGlyLeuTrpSerLeuCysTrpSerLeu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      71 ATGGCTAGGGTACTGGGAGCACCCGTTGCACTGGGGTTGTGGAGCCTATGCTGGTCTCTG 130

Qy      21 AlaIleAlaThrProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGluThr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     131 GCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTGCTGAAGGCGAGACC 190

Qy      41 LysProAspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAlaThrThr 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     191 AAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCTTTGATGCTACCACC 250

Qy      61 LeuAspAspAsnGlyThrMetLeuPhePheLysGlyGluPheValTrpLysSerHisLys 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     251 CTGGATGACAATGGAACCATGCTGTTTTTAAAGGGGAGTTTGTGTGGAAGAGTCACAAA 310

Qy      81 TrpAspArgGluLeuIleSerGluArgTrpLysAsnPheProSerProValAspAlaAla 100
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 TGGGACCGGGAGTTAATCTCAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCA 370

Qy        101 PheArgGlnGlyHisAsnSerValPheLeuIleLysGlyAspLysValTrpValTyrPro 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 TTCCGTCAAGGTCACAACAGTGTCTTTCTGATCAAGGGGGACAAAGTCTGGGTATACCCT 430

Qy        121 ProGluLysLysGluLysGlyTyrProLysLeuLeuGlnAspGluPheProGlyIlePro 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 CCTGAAAAGAAGGAGAAAGGATACCCAAAGTTGCTCCAAGATGAATTTCCTGGAATCCCA 490

Qy        141 SerProLeuAspAlaAlaValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 TCCCCACTGGATGCAGCTGTGGAATGTCACCGTGGAGAATGTCAAGCTGAAGGCGTCCTC 550

Qy        161 PhePheGln--------------------------------------------------- 163
              |||||||||
Db        551 TTCTTCCAAGGTGACCGCGAGTGGTTCTGGGACTTGGCTACGGGAACCATGAAGGAGCGT 610

Qy        163 ------------------------------------------------------------ 163

Db        611 TCCTGGCCAGCTGTTGGGAACTGCTCCTCTGCCCTGAGATGGCTGGGCCGCTACTACTGC 670

Qy        163 ------------------------------------------------------------ 163

Db        671 TTCCAGGGTAACCAATTCCTGCGCTTCGACCCTGTCAGGGGAGAGGTGCCTCCCAGGTAC 730

Qy        164 ------------------------------------------GlyHisGlyHisArgAsn 169
                                                        ||||||||||||||||||
Db        731 CCGCGGGATGTCCGAGACTACTTCATGCCCTGCCCTGGCAGAGGCCATGGACACAGGAAT 790

Qy        170 GlyThrGlyHisGlyAsnSerThrHisHisGlyProGluTyrMetArgCysSerProHis 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        791 GGGACTGGCCATGGGAACAGTACCCACCATGGCCCTGAGTATATGCGCTGTAGCCCACAT 850

Qy        190 LeuValLeuSerAlaLeuThrSerAspAsnHisGlyAlaThrTyrAlaPheSerGlyThr 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        851 CTAGTCTTGTCTGCACTGACGTCTGACAACCATGGTGCCACCTATGCCTTCAGTGGGACC 910

Qy        210 HisTyrTrpArgLeuAspThrSerArgAspGlyTrpHisSerTrpProIleAlaHisGln 229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        911 CACTACTGGCGTCTGGACACCAGCCGGGATGGCTGGCATAGCTGGCCCATTGCTCATCAG 970

Qy        230 TrpProGlnGlyProSerAlaValAspAlaAlaPheSerTrpGluGluLysLeuTyrLeu 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        971 TGGCCCCAGGGTCCTTCAGCAGTGGATGCTGCCTTTTCCTGGGAAGAAAAACTCTATCTG 1030

Qy        250 ValGlnGlyThrGlnValTyrValPheLeuThrLysGlyGlyTyrThrLeuValSerGly 269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1031 GTCCAGGGCACCCAGGTATATGTCTTCCTGACAAAGGGAGGCTATACCCTAGTAAGCGGT 1090

Qy        270 TyrProLysArgLeuGluLysGluValGlyThrProHisGlyIleIleLeuAspSerVal 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1091 TATCCGAAGCGGCTGGAGAAGGAAGTCGGGACCCCTCATGGGATTATCCTGGACTCTGTG 1150

Qy        290 AspAlaAlaPheIleCysProGlySerSerArgLeuHisIleMetAlaGlyArgArgLeu 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1151 GATGCGGCCTTTATCTGCCCTGGGTCTTCTCGGCTCCATATCATGGCAGGACGGCGGCTG 1210

Qy        310 TrpTrpLeuAspLeuLysSerGlyAlaGlnAlaThrTrpThrGluLeuProTrpProHis 329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1211 TGGTGGCTGGACCTGAAGTCAGGAGCCCAAGCCACGTGGACAGAGCTTCCTTGGCCCCAT 1270

Qy        330 GluLysValAspGlyAlaLeuCysMetGluLysSerLeuGlyProAsnSerCysSerAla 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1271 GAGAAGGTAGACGGAGCCTTGTGTATGGAAAAGTCCCTTGGCCCTAACTCATGTTCCGCC 1330

Qy        350 AsnGlyProGlyLeuTyrLeuIleHisGlyProAsnLeuTyrCysTyrSerAspValGlu 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1331 AATGGTCCCGGCTTGTACCTCATCCATGGTCCCAATTTGTACTGCTACAGTGATGTGGAG 1390

Qy        370 LysLeuAsnAlaAlaLysAlaLeuProGlnProGlnAsnValThrSerLeuLeuGlyCys 389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1391 AAACTGAATGCAGCCAAGGCCCTTCCGCAACCCCAGAATGTGACCAGTCTCCTGGGCTGC 1450

Qy        390 ThrHis 391
              ||||||
Db       1451 ACTCAC 1456

RESULT 4
US-10-175-523-84
; Sequence 84, Application US/10175523
; Publication No. US20030096264A1
; GENERAL INFORMATION:
;  APPLICANT: Brockman, Jeffrey
;  APPLICANT:  Evans, David
;  APPLICANT:  Hook, Derek
;  APPLICANT:  Klimczak, Leszek
;  APPLICANT:  Laeng, Pascal
;  APPLICANT:  Palfreyman, Michael
;  APPLICANT:  Rajan, Prithi
;  TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
;  FILE REFERENCE: 3235/1J795-US3
;  CURRENT APPLICATION NUMBER: US/10/175,523
;  CURRENT FILING DATE:  2002-06-18
;  PRIOR APPLICATION NUMBER: US 60/299,151
;  PRIOR FILING DATE: 2001-06-18
;  PRIOR APPLICATION NUMBER: US 60/317,828
;  PRIOR FILING DATE: 2001-09-07
;  PRIOR APPLICATION NUMBER: US 60/325,150
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US 60/333,047
;  PRIOR FILING DATE: 2001-11-14
;  PRIOR APPLICATION NUMBER: US 60/349,936
;  PRIOR FILING DATE: 2002-01-18
;  PRIOR APPLICATION NUMBER: US 60/361,834
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
;   LENGTH: 1516
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-175-523-84

Alignment Scores:
Pred. No.:              1.29e-161      Length:         1516
Score:                  1556.50        Matches:        296
Percent Similarity:     71.34%         Conservative:   35
Best Local Similarity:  63.79%         Mismatches:     54
Query Match:            71.24%         Indels:         79
DB:                     15             Gaps:           6

US-09-900-448-2 (1-391) x US-10-175-523-84 (1-1516)

Qy          1 MetAlaArgValLeuGlyAlaProValAlaLeuGlyLeuTrpSerLeuCysTrpSerLeu 20
              |||||||||   :::   |||         |||   |||      |||||||||||||||
Db         55 ATGGCTAGGACAGTAGTAGCACTAAATATCCTGGTATTGCTGGGCCTGTGCTGGTCCCTG 114

Qy         21 AlaIleAlaThrProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGlu--- 39
              |||:::|||   |||||||||      :::||||||      ||||||:::||||||
Db        115 GCTGTTGCCAACCCTCTTCCT------GCTGCCCATGAGACTGTTGCTAAAGGTGAAAAT 168

Qy         40 ---ThrLysProAspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAla 58
                 ||||||||||||   ||||||   |||   |||||||||   |||||||||||||||
Db        169 GGGACCAAGCCAGACTCAGATGTAATCGAACACTGCTCAGATGCCTGGAGCTTTGACGCT 228

Qy         59 ThrThrLeuAspAspAsnGlyThrMetLeuPhePheLysGlyGluPheValTrpLysSer 78
              ||||||:::|||   |||||||||||||||||||||||||||||||||||||||:::
Db        229 ACCACCATGGATCACAATGGGACCATGCTGTTCTTTAAAGGGGAGTTTGTGTGGAGGGGT 288

Qy         79 HisLysTrpAspArgGluLeuIleSerGluArgTrpLysAsnPheProSerProValAsp 98
              |||         ||||||||||||||||||||||||||||||      :::   ||||||
Db        289 CACTCAGGGATCCGGGAGTTAATCTCAGAGAGGTGGAAGAATCCCGTCACCTCAGTGGAT 348

Qy         99 AlaAlaPheArgGlnGlyHisAsnSerValPheLeuIleLysGlyAspLysValTrpVal 118
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              ||||||||||||   |||   :::||||||||||||||||||   |||||||||||||||
Db        349 GCTGCATTCCGT---GGTCCTGACAGTGTCTTCCTGATCAAGGAAGACAAAGTCTGGGTG 405

Qy        119 TyrProProGluLysLysGluLysGlyTyrProLysLeuLeuGlnAspGluPheProGly 138
              |||||||||||||||||||||   |||||||||||||||   |||:::|||   ||||||
Db        406 TATCCTCCTGAAAAGAAAGAGAACGGGTATCCAAAGTTGTTCCAAGAAGAGTCTCCTGGA 465

Qy        139 IleProSerProLeuAspAlaAlaValGluCysHisArgGlyGluCysGlnAlaGluGly 158
              ||||||   |||   ||||||||||||||||||||||||||||||||||||:::||||||
Db        466 ATCCCATACCCACCAGACGCAGCTGTGGAATGCCACCGTGGAGAATGCCAGAGTGAAGGT 525

Qy        159 ValLeuPhePheGlnGlyHis--------------------------------------- 165
              ||||||||||||||||||:::
Db        526 GTCCTCTTCTTCCAAGGTAACCGCAAGTGGTTCTGGGACTTTGCCACAAGAACCCAAAAG 585

Qy        165 ------------------------------------------------------------ 165

Db        586 GAACGTTCCTGGCCTGCTGTTGGGAATTGCACTGCGGCCTTGAGGTGGCTTGAACGCTAC 645

Qy        165 ------------------------------------------------------------ 165

Db        646 TACTGCTTCCAGGGTAACAAGTTCCTGAGATTTAACCCCGTCACAGGAGAGGTGCCTCCC 705

Qy        166 ------------------------------------------------GlyHis------ 167
                                                              ||||||
Db        706 AGATACCCTCTGGATGCCCGTGACTACTTCATATCCTGCCCTGGCAGAGGCCATGGTAAA 765

Qy        168 ---ArgAsnGlyThrGlyHisGlyAsnSerThrHisHisGlyProGluTyrMetArgCys 186
                 ||||||||||||   ||||||||||||||||||      |||   :::   ||||||
Db        766 CTAAGAAATGGAACTGCTCATGGGAATAGCACCCAT------CCTATGCATTCGCGTTGT 819

Qy        187 SerProHisLeuValLeuSerAlaLeuThrSerAspAsnHisGlyAlaThrTyrAlaPhe 206
              :::            ||||||||||||   ||||||:::   ||||||||||||||||||
Db        820 AACGCAGATCCTGGCCTGTCTGCACTGCTGTCTGACCATCGAGGTGCCACCTATGCCTTC 879

Qy        207 SerGlyThrHisTyrTrpArgLeuAspThrSerArgAspGlyTrpHisSerTrpProIle 226
              ||||||:::||||||||||||||||||:::||||||||||||||||||||||||||||||
Db        880 AGTGGCTCCCACTACTGGCGTCTGGACTCCAGCCGTGATGGGTGGCATAGCTGGCCCATT 939

Qy        227 AlaHisGlnTrpProGlnGlyProSerAlaValAspAlaAlaPheSerTrpGluGluLys 246
              ||||||   ||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        940 GCTCATCACTGGCCCCAGGGTCCTTCAGCAGTAGATGCTGCCTTTTCCTGGGATGAGAAA 999

Qy        247 LeuTyrLeuValGlnGlyThrGlnValTyrValPheLeuThrLysGlyGlyTyrThrLeu 266
              :::||||||:::|||||||||||||||||||||||||||||||||||||||      |||
Db       1000 GTCTATCTGATCCAGGGCACTCAAGTATATGTCTTCCTGACGAAGGGGGGCAATAACCTA 1059

Qy        267 ValSerGlyTyrProLysArgLeuGluLysGluValGlyThrProHisGlyIleIleLeu 286
              |||||||||||||||||||||||||||||||||:::|||:::|||   ||||||   |||
Db       1060 GTAAGTGGTTATCCAAAGCGGCTGGAGAAGGAACTTGGGAGCCCTCCCGGGATCAGCCTT 1119

Qy        287 AspSerValAspAlaAlaPheIleCysProGlySerSerArgLeuHisIleMetAlaGly 306
              |||::::::||||||||||||   |||||||||||||||:::|||::::::   :::|||
Db       1120 GATACCATAGATGCAGCCTTTTCCTGCCCTGGTTCTTCCAAGCTCTACGTCACATCAGGA 1179

Qy        307 ArgArgLeuTrpTrpLeuAspLeuLysSerGlyAlaGlnAlaThrTrpThrGluLeuPro 326
              ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db       1180 CGGCGGCTTTGGTGGCTGGACCTGAAGTCAGGAGCCCAGGCGACATGGGCAGAGCTTTCC 1239

Qy        327 TrpProHisGluLysValAspGlyAlaLeuCysMetGluLysSerLeuGlyProAsnSer 346
              |||||||||||||||||||||||||||||||||:::||||||||||||||||||   |||
Db       1240 TGGCCCCATGAGAAAGTTGATGGTGCCCTGTGTTTGGAAAAGTCCCTTGGTCCCTACTCA 1299

Qy        347 CysSerAlaAsnGlyProGlyLeuTyrLeuIleHisGlyProAsnLeuTyrCysTyrSer 366
              ||||||:::|||||||||   |||:::   ||||||||||||||||||||||||||||||
Db       1300 TGCTCTTCCAATGGTCCCAACTTGTTCTTTATCCATGGCCCAATTTATACTGCTATAGC 1359

Qy        367 AspValGluLysLeuAsnAlaAlaLysAlaLeuProGlnProGlnAsnValThrSerLeu 386
                 ::::::||||||||||||||||||:::|||||||||||||||   |||   |||:::
Db       1360 AGTATAGACAAACTGAATGCAGCCAAGAGTCTGCCTCAGCCCCAGAAAGTGAACAGCATC 1419

Qy        387 LeuGlyCysThr 390
              |||||||||:::
```

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Db       1420 CTTGGCTGCAGT 1431

RESULT 5
US-10-316-253-39
; Sequence 39, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
;  APPLICANT: The Procter & Gamble Company
;  APPLICANT:  Peters, Kevin
;  APPLICANT:  Thompson, Larry
;  APPLICANT:  Wang, Feng
;  APPLICANT:  Greis, Kenneth
;  TITLE OF INVENTION: Angiogenesis Modulating Proteins
;  FILE REFERENCE: 8865M
;  CURRENT APPLICATION NUMBER: US/10/316,253
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: US 60/355,295
;  PRIOR FILING DATE: 2002-02-08
;  NUMBER OF SEQ ID NOS: 308
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
;   LENGTH: 1516
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (55)..(1437)
;   OTHER INFORMATION:
US-10-316-253-39

Alignment Scores:
Pred. No.:              1.29e-161      Length:        1516
Score:                  1556.50        Matches:       296
Percent Similarity:     71.34%         Conservative:  35
Best Local Similarity:  63.79%         Mismatches:    54
Query Match:            71.24%         Indels:        79
DB:                     15             Gaps:          6

US-09-900-448-2 (1-391) x US-10-316-253-39 (1-1516)

Qy          1 MetAlaArgValLeuGlyAlaProValAlaLeuGlyLeuTrpSerLeuCysTrpSerLeu 20
              |||||||||   :::   |||         |||   |||      |||||||||||||||
Db         55 ATGGCTAGGACAGTAGTAGCACTAAATATCCTGGTATTGCTGGGCCTGTGCTGGTCCCTG 114

Qy         21 AlaIleAlaThrProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGlu--- 39
              |||:::|||   |||||||||      :::||||||      ||||||:::||||||
Db        115 GCTGTTGCCAACCCTCTTCCT------GCTGCCCATGAGACTGTTGCTAAAGGTGAAAAT 168

Qy         40 ---ThrLysProAspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAla 58
                 ||||||||||||   ||||||   |||   |||||||||   |||||||||||||||
Db        169 GGGACCAAGCCAGACTCAGATGTAATCGAACACTGCTCAGATGCCTGGAGCTTTGACGCT 228

Qy         59 ThrThrLeuAspAspAsnGlyThrMetLeuPhePheLysGlyGluPheValTrpLysSer 78
              ||||||:::|||   |||||||||||||||||||||||||||||||||||||||:::
Db        229 ACCACCATGGATCACAATGGACCATGCTGTTCTTTAAAGGGGAGTTTGTGTGGAGGGGT 288

Qy         79 HisLysTrpAspArgGluLeuIleSerGluArgTrpLysAsnPheProSerProValAsp 98
              |||         ||||||||||||||||||||||||||||||      :::   ||||||
Db        289 CACTCAGGGATCCGGGAGTTAATCTCAGAGAGGTGGAAGAATCCCGTCACCTCAGTGGAT 348

Qy         99 AlaAlaPheArgGlnGlyHisAsnSerValPheLeuIleLysGlyAspLysValTrpVal 118
              ||||||||||||   |||   :::||||||||||||||||||   |||||||||||||||
Db        349 GCTGCATTCCGT---GGTCCTGACAGTGTCTTCCTGATCAAGGAAGACAAAGTCTGGGTG 405

Qy        119 TyrProProGluLysLysGluLysGlyTyrProLysLeuLeuGlnAspGluPheProGly 138
              |||||||||||||||||||||   |||||||||||||||   |||:::|||   ||||||
Db        406 TATCCTCCTGAAAAGAAAGAGAACGGGTATCCAAAGTTGTTCCAAGAAGAGTCTCCTGGA 465

Qy        139 IleProSerProLeuAspAlaAlaValGluCysHisArgGlyGluCysGlnAlaGluGly 158
              ||||||   |||   ||||||||||||||||||||||||||||||||||||:::||||||
Db        466 ATCCCATACCCACCAGACGCAGCTGTGGAATGCCACCGTGGAGAATGCCAGAGTGAAGGT 525

Qy        159 ValLeuPhePheGlnGlyHis--------------------------------------- 165
```

```
              ||||||||||||||||||:::
Db        526 GTCCTCTTCTTCCAAGGTAACCGCAAGTGGTTCTGGGACTTTGCCACAAGAACCCAAAAG 585

Qy        165 ------------------------------------------------------------ 165

Db        586 GAACGTTCCTGGCCTGCTGTTGGGAATTGCACTGCGGCCTTGAGGTGGCTTGAACGCTAC 645

Qy        165 ------------------------------------------------------------ 165

Db        646 TACTGCTTCCAGGGTAACAAGTTCCTGAGATTTAACCCCGTCACAGGAGAGGTGCCTCCC 705

Qy        166 ------------------------------------------------GlyHis------ 167
                                                              ||||||
Db        706 AGATACCCTCTGGATGCCCGTGACTACTTCATATCCTGCCCTGGCAGAGGCCATGGTAAA 765

Qy        168 ---ArgAsnGlyThrGlyHisGlyAsnSerThrHisHisGlyProGluTyrMetArgCys 186
                 ||||||||||||   ||||||||||||||||||      |||   :::   ||||||
Db        766 CTAAGAAATGGAACTGCTCATGGGAATAGCACCCAT------CCTATGCATTCGCGTTGT 819

Qy        187 SerProHisLeuValLeuSerAlaLeuThrSerAspAsnHisGlyAlaThrTyrAlaPhe 206
              :::            ||||||||||||   ||||||:::   ||||||||||||||||||
Db        820 AACGCAGATCCTGGCCTGTCTGCACTGCTGTCTGACCATCGAGGTGCCACCTATGCCTTC 879

Qy        207 SerGlyThrHisTyrTrpArgLeuAspThrSerArgAspGlyTrpHisSerTrpProIle 226
              ||||||:::||||||||||||||||||:::||||||||||||||||||||||||||||||
Db        880 AGTGGCTCCCACTACTGGCGTCTGGACTCCAGCCGTGATGGGTGGCATAGCTGGCCCATT 939

Qy        227 AlaHisGlnTrpProGlnGlyProSerAlaValAspAlaAlaPheSerTrpGluGluLys 246
              ||||||   ||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        940 GCTCATCACTGGCCCCAGGGTCCTTCAGCAGTAGATGCTGCCTTTTCCTGGGATGAGAAA 999

Qy        247 LeuTyrLeuValGlnGlyThrGlnValTyrValPheLeuThrLysGlyGlyTyrThrLeu 266
              :::||||||:::|||||||||||||||||||||||||||||||||||||||      |||
Db       1000 GTCTATCTGATCCAGGGCACTCAAGTATATGTCTTCCTGACGAAGGGGGGCAATAACCTA 1059

Qy        267 ValSerGlyTyrProLysArgLeuGluLysGluValGlyThrProHisGlyIleIleLeu 286
              |||||||||||||||||||||||||||||||||:::|||:::|||   ||||||   |||
Db       1060 GTAAGTGGTTATCCAAAGCGGCTGGAGAAGGAACTTGGGAGCCCTCCCGGGATCAGCCTT 1119

Qy        287 AspSerValAspAlaAlaPheIleCysProGlySerSerArgLeuHisIleMetAlaGly 306
              |||::::::||||||||||||   |||||||||||||||:::|||::::::   :::|||
Db       1120 GATACCATAGATGCAGCCTTTTCCTGCCCTGGTTCTTCCAAGCTCTACGTCACATCAGGA 1179

Qy        307 ArgArgLeuTrpTrpLeuAspLeuLysSerGlyAlaGlnAlaThrTrpThrGluLeuPro 326
              ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db       1180 CGGCGGCTTTGGTGGCTGGACCTGAAGTCAGGAGCCCAGGCGACATGGGCAGAGCTTTCC 1239

Qy        327 TrpProHisGluLysValAspGlyAlaLeuCysMetGluLysSerLeuGlyProAsnSer 346
              |||||||||||||||||||||||||||||||||:::||||||||||||||||||   |||
Db       1240 TGGCCCCATGAGAAAGTTGATGGTGCCCTGTGTTTGGAAAAGTCCCTTGGTCCCTACTCA 1299

Qy        347 CysSerAlaAsnGlyProGlyLeuTyrLeuIleHisGlyProAsnLeuTyrCysTyrSer 366
              ||||||:::|||||||||   |||:::   ||||||||||||||||||||||||||||||
Db       1300 TGCTCTTCCAATGGTCCCAACTTGTTCTTTATCCATGGGCCCAATTTATACTGCTATAGC 1359

Qy        367 AspValGluLysLeuAsnAlaAlaLysAlaLeuProGlnProGlnAsnValThrSerLeu 386
                 ::::::||||||||||||||||||:::|||||||||||||||   |||   |||:::
Db       1360 AGTATAGACAAACTGAATGCAGCCAAGAGTCTGCCTCAGCCCCAGAAAGTGAACAGCATC 1419

Qy        387 LeuGlyCysThr 390
              |||||||||:::
Db       1420 CTTGGCTGCAGT 1431

RESULT 6
US-10-162-335-87
; Sequence 87, Application US/10162335
; Publication No. US20040009480A1
; GENERAL INFORMATION:
;  APPLICANT: Anderson, David W.
;  APPLICANT:  Baumgartner, Jason C.
;  APPLICANT:  Boldog, Ferenc L.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Hjalt, Tord
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Li, Li
;  APPLICANT:  MacDougall, John R.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Pena, Carol E. A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Stone, David J.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Vernet, Corine A. M.
;  APPLICANT:  Voss, Edward Z.
;  APPLICANT:  Zerhusen, Bryan D.
;  TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
;  FILE REFERENCE: 21402-377 B
;  CURRENT APPLICATION NUMBER: US/10/162,335
;  CURRENT FILING DATE:  2002-10-01
;  PRIOR APPLICATION NUMBER: 60/295,607
;  PRIOR FILING DATE: 2001-06-04
;  PRIOR APPLICATION NUMBER: 60/295,661
;  PRIOR FILING DATE: 2001-06-04
;  PRIOR APPLICATION NUMBER: 60/296,404
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: 60/296,418
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: 60/297,414
;  PRIOR FILING DATE: 2001-06-11
;  PRIOR APPLICATION NUMBER: 60/297,567
;  PRIOR FILING DATE: 2001-06-12
;  PRIOR APPLICATION NUMBER: 60/298,285
;  PRIOR FILING DATE: 2001-06-14
;  PRIOR APPLICATION NUMBER: 60/298,556
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/299,949
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/300,883
;  PRIOR FILING DATE: 2001-06-26
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 201
; SEQ ID NO 87
;   LENGTH: 861
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (10)..(775)
US-10-162-335-87

Alignment Scores:
Pred. No.:              7.92e-138       Length:         861
Score:                  1338.00         Matches:        255
Percent Similarity:     65.22%          Conservative:   0
Best Local Similarity:  65.22%          Mismatches:     0
Query Match:            61.24%          Indels:         136
DB:                     16              Gaps:           1

US-09-900-448-2 (1-391) x US-10-162-335-87 (1-861)

Qy          1 MetAlaArgValLeuGlyAlaProValAlaLeuGlyLeuTrpSerLeuCysTrpSerLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 ATGGCTAGGGTACTGGGAGCACCCGTTGCACTGGGGTTGTGGAGCCTATGCTGGTCTCTG 69

Qy         21 AlaIleAlaThrProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGluThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 GCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTGCTGAAGGCGAGACC 129
```

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Qy          41 LysProAspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAlaThrThr 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         130 AAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCTTTGATGCTACCACC 189

Qy          61 LeuAspAspAsnGlyThrMetLeuPhePheLysGlyGluPheValTrpLysSerHisLys 80
               |||||||||||||||||||||||||||||||||
Db         190 CTGGATGACAATGGAACCATGCTGTTTTTTAAA--------------------------- 222

Qy          81 TrpAspArgGluLeuIleSerGluArgTrpLysAsnPheProSerProValAspAlaAla 100

Db         222 ------------------------------------------------------------ 222

Qy         101 PheArgGlnGlyHisAsnSerValPheLeuIleLysGlyAspLysValTrpValTyrPro 120

Db         222 ------------------------------------------------------------ 222

Qy         121 ProGluLysLysGluLysGlyTyrProLysLeuLeuGlnAspGluPheProGlyIlePro 140

Db         222 ------------------------------------------------------------ 222

Qy         141 SerProLeuAspAlaAlaValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeu 160

Db         222 ------------------------------------------------------------ 222

Qy         161 PhePheGlnGlyHisGlyHisArgAsnGlyThrGlyHisGlyAsnSerThrHisHisGly 180

Db         222 ------------------------------------------------------------ 222

Qy         181 ProGluTyrMetArgCysSerProHisLeuValLeuSerAlaLeuThrSerAspAsnHis 200

Db         222 ------------------------------------------------------------ 222

Qy         201 GlyAlaThrTyrAlaPheSerGlyThrHisTyrTrpArgLeuAspThrSerArgAspGly 220
                                    |||||||||||||||||||||||||||||||||||||||
Db         223 ---------------------GGGACCCACTACTGGCGTCTGGACACCAGCCGGGATGGC 261

Qy         221 TrpHisSerTrpProIleAlaHisGlnTrpProGlnGlyProSerAlaValAspAlaAla 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         262 TGGCATAGCTGGCCCATTGCTCATCAGTGGCCCCAGGGTCCTTCAGCAGTGGATGCTGCC 321

Qy         241 PheSerTrpGluGluLysLeuTyrLeuValGlnGlyThrGlnValTyrValPheLeuThr 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         322 TTTTCCTGGGAAGAAAAACTCTATCTGGTCCAGGGCACCCAGGTATATGTCTTCCTGACA 381

Qy         261 LysGlyGlyTyrThrLeuValSerGlyTyrProLysArgLeuGluLysGluValGlyThr 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         382 AAGGGAGGCTATACCCTAGTAAGCGGTTATCCGAAGCGGCTGGAGAAGGAAGTCGGGACC 441

Qy         281 ProHisGlyIleIleLeuAspSerValAspAlaAlaPheIleCysProGlySerSerArg 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         442 CCTCATGGGATTATCCTGGACTCTGTGGATGCGGCCTTTATCTGCCCTGGGTCTTCTCGG 501

Qy         301 LeuHisIleMetAlaGlyArgArgLeuTrpTrpLeuAspLeuLysSerGlyAlaGlnAla 320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         502 CTCCATATCATGGCAGGACGGCGGCTGTGGTGGCTGGACCTGAAGTCAGGAGCCCAAGCC 561

Qy         321 ThrTrpThrGluLeuProTrpProHisGluLysValAspGlyAlaLeuCysMetGluLys 340
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         562 ACGTGGACAGAGCTTCCTTGGCCCCATGAGAAGGTAGACGGAGCCTTGTGTATGGAAAAG 621

Qy         341 SerLeuGlyProAsnSerCysSerAlaAsnGlyProGlyLeuTyrLeuIleHisGlyPro 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         622 TCCCTTGGCCCTAACTCATGTTCCGCCAATGGTCCCGGCTTGTACCTCATCCATGGTCCC 681

Qy         361 AsnLeuTyrCysTyrSerAspValGluLysLeuAsnAlaAlaLysAlaLeuProGlnPro 380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         682 AATTTGTACTGCTACAGTGATGTGGAGAAACTGAATGCAGCCAAGGCCCTTCCGCAACCC 741

Qy         381 GlnAsnValThrSerLeuLeuGlyCysThrHis 391
               |||||||||||||||||||||||||||||||||
Db         742 CAGAATGTGACCAGTCTCCTGGGCTGCACTCAC 774
```

RESULT 7

```
US-09-900-448-3
; Sequence 3, Application US/09900448
; Publication No. US20030220488A1
; GENERAL INFORMATION:
;  APPLICANT: CECCARDI, Toni et al.
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
;  TITLE OF INVENTION: USES THEREOF
;  FILE REFERENCE: CL001272
;  CURRENT APPLICATION NUMBER: US/09/900,448
;  CURRENT FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 13737
;   TYPE: DNA
;   ORGANISM: Human
US-09-900-448-3

Alignment Scores:
Pred. No.:              2.74e-90        Length:         13737
Score:                  921.00          Matches:        195
Percent Similarity:     53.91%          Conservative:   5
Best Local Similarity:  52.56%          Mismatches:     27
Query Match:            42.15%          Indels:         146
DB:                     11              Gaps:           6

US-09-900-448-2 (1-391) x US-09-900-448-3 (1-13737)

Qy         165 HisGlyHisArgAsnGlyThrGlyHisGlyAsnSerThrHisHisGlyPro--------- 181
               |||||||||            |||               |||
Db       10628 CATGGACACCTGAAATCCTTAGGGAGTGCCCGCCAACCCCATGATGTTGGCCTTACCTGG 10687

Qy         182 GluTyrMetArgCysSerProHisLeuValLeuSerAlaLeuThrSerAsp--------- 198
               :::         |||   |||||||||                  :::|||
Db       10688 AAACTTAGCCACTGTTTTCCACACTTGCCTTTCTTTCAGGCACCTGCTGATTCCAGTTTC 10747

Qy         199 AsnHisGlyAlaThr------------------------------TyrAlaPheSer--- 207
               :::   |||                                    ::::::||||||
Db       10748 AGCCAGGGCACAGTGCCCAACATTGCTGACCAAGTCTTGCTCTATTTCTCCTTCTCACCT 10807

Qy         207 ------------------------------------------------------------ 207

Db       10808 GGCCTCTTCCATCTTGGCCTCTGGATGCATTCTCTCCCTCTCATGACTCATTTCTGCATT 10867

Qy         207 ------------------------------------------------------------ 207

Db       10868 CATCACTAGCCTCTTCTCTGCCTGGGCTTCTGCCAGCGGCCCTAGAGCAACCTATGGTAT 10927

Qy         208 ------GlyThrHisTyrTrpArgLeuAspThrSerArgAspGlyTrpHisSerTrpPro 225
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       10928 TCCACAGGGACCCACTACTGGCGTCTGGACACCAGCCGGGATGGCTGGCATAGCTGGCCC 10987

Qy         226 IleAlaHisGlnTrpProGlnGlyProSerAlaValAspAlaAlaPheSerTrpGluGlu 245
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       10988 ATTGCTCATCAGTGGCCCCAGGGTCCTTCAGCAGTGGATGCTGCCTTTTCCTGGGAAGAA 11047

Qy         246 LysLeuTyrLeuVal--------------------------------------------- 250
               ||||||||||||
Db       11048 AAACTCTATCTGGT-CCAGGTGTGTATTGGGGGAGAGGCTTGAGGTAGAGACTGGGACAA 11106

Qy         251 ---------------------------------------GlnGlyThrGlnValTyrVal 257
                                                      |||||||||||||||||||||
Db       11107 GCATATCCAACTCTGTATTTATTACCATCCTTTGTCCTCCAGGGCACCCAGGTATATGTC 11166

Qy         258 PheLeuThrLysGlyGlyTyrThrLeuValSerGlyTyrProLysArgLeuGluLysGlu 277
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       11167 TTCCTGACAAAGGGAGGCTATACCCTAGTAAGCGGTTATCCGAAGCGGCTGGAGAAGGAA 11226

Qy         278 ValGlyThrProHisGlyIleIleLeuAspSerValAspAlaAlaPheIleCysProGly 297
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       11227 GTCGGGACCCCTCATGGGATTATCCTGGACTCTGTGGATGCGGCCTTTATCTGCCCTGGG 11286
```

```
Qy          298 SerSerArgLeuHisIleMetAla------------------------------------ 305
                ||||||||||||||||||||||||
Db        11287 TCTTCTCGGCTCCATATCATGGC-AGGTGAGGGGCTTCTGGGTGCTTAGAGGGCAGCTTG 11345

Qy          305 ------------------------------------------------------------ 305

Db        11346 TTCTGCTACCTGTCTGTGGCATAGATCCCCACCAGGGCATGAGAAGGCCTAGGTCAGGAT 11405

Qy          305 ------------------------------------------------------------ 305

Db        11406 CCCCAGGGCATGAGAAGGCCTAGGTCAGGATCCCCATGACATGGAAGCCATGCTATGTTT 11465

Qy          306 ---------------GlyArgArgLeuTrpTrpLeuAspLeuLysSerGlyAlaGlnAla 320
                               |||||||||||||||||||||||||||||||||||||||||||||
Db        11466 GGTGCCTTCTCCCCAGGACGGCGGCTGTGGTGGCTGGACCTGAAGTCAGGAGCCCAAGCC 11525

Qy          321 ThrTrpThrGluLeuProTrpProHisGluLysValAspGlyAlaLeuCysMetGluLys 340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        11526 ACGTGGACAGAGCTTCCTTGGCCCCATGAGAAGGTAGACGGAGCCTTGTGTATGGAAAAG 11585

Qy          341 SerLeuGlyProAsnSerCysSerAlaAsnGlyProGlyLeuTyrLeuIleHisGlyPro 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        11586 TCCCTTGGCCCTAACTCATGTTCCGCCAATGGTCCCGGCTTGTACCTCATCCATGGTCCC 11645

Qy          361 AsnLeuTyrCysTyrSerAspValGluLysLeuAsnAlaAlaLysAlaLeuProGlnPro 380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        11646 AATTTGTACTGCTACAGTGATGTGGAGAAACTGAATGCAGCCAAGGCCCTTCCGCAACCC 11705

Qy          381 GlnAsnValThrSerLeuLeuGlyCysThrHis 391
                |||||||||||||||||||||||||||||||||
Db        11706 CAGAATGTGACCAGTCTCCTGGGCTGCACTCAC 11738

RESULT 8
US-09-918-995-30828
; Sequence 30828, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 30828
;   LENGTH: 488
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(488)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-30828

Alignment Scores:
Pred. No.:              1.33e-75        Length:         488
Score:                  771.00          Matches:        139
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            35.29%          Indels:         0
DB:                     10              Gaps:           0

US-09-900-448-2 (1-391) x US-09-918-995-30828 (1-488)

Qy            1 MetAlaArgValLeuGlyAlaProValAlaLeuGlyLeuTrpSerLeuCysTrpSerLeu 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           71 ATGGCTAGGGTACTGGGAGCACCCGTTGCACTGGGGTTGTGGAGCCTATGCTGGTCTCTG 130

Qy           21 AlaIleAlaThrProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGluThr 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          131 GCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTGCTGAAGGCGAGACC 190

Qy           41 LysProAspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAlaThrThr 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          191 AAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCTTTGATGCTACCACC 250

Qy           61 LeuAspAspAsnGlyThrMetLeuPhePheLysGlyGluPheValTrpLysSerHisLys 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          251 CTGGATGACAATGGAACCATGCTGTTTTTTAAAGGGGAGTTTGTGTGGAAGAGTCACAAA 310

Qy           81 TrpAspArgGluLeuIleSerGluArgTrpLysAsnPheProSerProValAspAlaAla 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          311 TGGGACCGGGAGTTAATCTCAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCA 370

Qy          101 PheArgGlnGlyHisAsnSerValPheLeuIleLysGlyAspLysValTrpValTyrPro 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          371 TTCCGTCAAGGTCACAACAGTGTCTTTCTGATCAAGGGGGACAAAGTCTGGGTATACCCT 430

Qy          121 ProGluLysLysGluLysGlyTyrProLysLeuLeuGlnAspGluPheProGlyIle 139
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          431 CCTGAAAAGAAGGAGAAAGGATACCCAAAGTTGCTCCAAGATGAATTTCCTGGAATC 487

RESULT 9
US-09-918-995-8595
; Sequence 8595, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8595
;   LENGTH: 422
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-918-995-8595

Alignment Scores:
Pred. No.:              8.29e-74        Length:         422
Score:                  754.00          Matches:        136
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            34.51%          Indels:         0
DB:                     10              Gaps:           0

US-09-900-448-2 (1-391) x US-09-918-995-8595 (1-422)

Qy            1 MetAlaArgValLeuGlyAlaProValAlaLeuGlyLeuTrpSerLeuCysTrpSerLeu 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           14 ATGGCTAGGGTACTGGGAGCACCCGTTGCACTGGGGTTGTGGAGCCTATGCTGGTCTCTG 73

Qy           21 AlaIleAlaThrProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGluThr 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           74 GCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTGCTGAAGGCGAGACC 133

Qy           41 LysProAspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAlaThrThr 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          134 AAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCTTTGATGCTACCACC 193

Qy           61 LeuAspAspAsnGlyThrMetLeuPhePheLysGlyGluPheValTrpLysSerHisLys 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          194 CTGGATGACAATGGAACCATGCTGTTTTTTAAAGGGGAGTTTGTGTGGAAGAGTCACAAA 253

Qy           81 TrpAspArgGluLeuIleSerGluArgTrpLysAsnPheProSerProValAspAlaAla 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          254 TGGGACCGGGAGTTAATCTCAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCA 313
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Qy         101 PheArgGlnGlyHisAsnSerValPheLeuIleLysGlyAspLysValTrpValTyrPro 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         314 TTCCGTCAAGGTCACAACAGTGTCTTTCTGATCAAGGGGGACAAAGTCTGGGTATACCCT 373

Qy         121 ProGluLysLysGluLysGlyTyrProLysLeuLeuGlnAspGluPhe 136
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db         374 CCTGAAAAGAAGGAGAAAGGATACCCAAAGTTGCTCCAAGATGAATTT 421

RESULT 10
US-09-918-995-31395
; Sequence 31395, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31395
;   LENGTH: 492
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(492)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31395

Alignment Scores:
Pred. No.:               2.61e-69      Length:         492
Score:                   714.00        Matches:        135
Percent Similarity:      93.84%        Conservative:   2
Best Local Similarity:   92.47%        Mismatches:     9
Query Match:             32.68%        Indels:         1
DB:                      10            Gaps:           0

US-09-900-448-2 (1-391) x US-09-918-995-31395 (1-492)

Qy           1 MetAlaArgValLeuGlyAlaProValAlaLeuGlyLeuTrpSerLeuCysTrpSerLeu 20
               ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db          56 ATGGCTAGGGTACTGGAGCACCCGATGCACTGGGGTTGTGGAGCCTATGCTGGTCTCTG 115

Qy          21 AlaIleAlaThrProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGluThr 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         116 GCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTGCTGAAGGCGAGACC 175

Qy          41 LysProAspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAlaThrThr 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         176 AAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCTTTGATGCTACCACC 235

Qy          61 LeuAspAspAsnGlyThrMetLeuPhePheLysGlyGluPheValTrpLysSerHisLys 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         236 CTGGATGACAATGGAACCATGCTGTTTTTTAAAGGGGAGTTTGTGTGGAAGAGTCACAAA 295

Qy          81 TrpAspArgGluLeuIleSerGluArgTrpLysAsnPheProSerProValAspAlaAla 100
               |||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db         296 TGGGACCGGGAGTTAATCTCACAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCA 355

Qy         101 PheArgGlnGlyHisAsnSerValPheLeuIleLysGlyAspLysValTrpValTyrPro 120
               ||||||||||||||||||||||||||||||||||||||||||   |||   |||||||||
Db         356 TTCCGTCAAGGTCACAACAGTGTCTTTCTGATCAAGGGGGACACAGTCTGAGTATACCCT 415

Qy         121 ProGluLysLysGluLysGlyTyrProLysLeuLeuGlnAspGluPheProGlyIlePro 140
               |||      ||||||   ||||||||||||:::|||||||||||||||   |||   |||
Db         416 CCTGANNAGAAGGAGACAGGATACCCAAAAGTGCTCCAAGATGAATTCACTGGATC-CCA 474

Qy         141 SerProLeuAspAlaAla 146
                  |||||||||||||||
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Db         475 TACCCACTGGATGCAGCN 492

RESULT 11
US-09-918-995-30754
; Sequence 30754, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 30754
;   LENGTH: 488
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(488)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-30754

Alignment Scores:
Pred. No.:               9.19e-69      Length:         488
Score:                   709.00        Matches:        130
Percent Similarity:      80.00%        Conservative:   6
Best Local Similarity:   76.47%        Mismatches:     8
Query Match:             32.45%        Indels:         26
DB:                      10            Gaps:           2

US-09-900-448-2 (1-391) x US-09-918-995-30754 (1-488)

Qy         120 ProProGluLysLysGluLysGlyTyrProLysLeuLeuGlnAspGluPheProGlyIle 139
               ||||||                  ||||||:::   ::::::|||   |||
Db          57 CCTCCCAGG---------------TACCCGCGGGATGTCCGAGACTACTTCATGCCCTGC 101

Qy         140 ProSerProLeuAspAlaAlaValGluCysHisArgGlyGluCysGlnAlaGluGlyVal 159
               |||
Db         102 CCTGGC------------------------------------------------------ 107

Qy         160 LeuPhePheGlnGlyHisGlyHisArgAsnGlyThrGlyHisGlyAsnSerThrHisHis 179
                        :::||||||||||||||||||||||||||||||||||||||||||||||||
Db         108 ---------AGAGGCCATGGACACAGGAATGGGACTGGCCATGGGAACAGTACCCACCAT 158

Qy         180 GlyProGluTyrMetArgCysSerProHisLeuValLeuSerAlaLeuThrSerAspAsn 199
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         159 GGCCCTGAGTATATGCGCTGTAGCCCACATCTAGTCTTGTCTGCACTGACGTCTGACAAC 218

Qy         200 HisGlyAlaThrTyrAlaPheSerGlyThrHisTyrTrpArgLeuAspThrSerArgAsp 219
               ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db         219 CATGGTGCCACCTATGCCTTCAGTGGGACCCACTACTGGCGTATGGACACCAGCCGGGAT 278

Qy         220 GlyTrpHisSerTrpProIleAlaHisGlnTrpProGlnGlyProSerAlaValAspAla 239
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         279 GGCTGGCATAGCTGGCCCATTGCTCATCAGTGGCCCCAGGGTCCTTCAGCAGTGGATGCT 338

Qy         240 AlaPheSerTrpGluGluLysLeuTyrLeuValGlnGlyThrGlnValTyrValPheLeu 259
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         339 GCCTTTTCCTGGGAAGAAAAACTCTATCTGGTCCAGGGCACCCAGGTATATGTCTTCCTG 398

Qy         260 ThrLysGlyGlyTyrThrLeuValSerGlyTyrProLysArgLeuGluLysGluValGly 279
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db         399 ACAAAGGGAGGCTATACCCTAGTAAGCGGTTATCCGAAGCGGCTGGAGAAGGAAGACGGG 458

Qy         280 ThrProHisGlyIleIleLeuAspSerVal 289
               |||||||||||||||:::||||||||||||
Db         459 ACCCCTCATGGGATTATGCTGGACTCTGTG 488
```

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RESULT 12
US-09-918-995-32820
; Sequence 32820, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32820
;   LENGTH: 491
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(491)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32820

Alignment Scores:
Pred. No.:                1.1e-63      Length:        491
Score:                    663.00       Matches:       122
Percent Similarity:       79.25%       Conservative:  4
Best Local Similarity:    76.73%       Mismatches:    7
Query Match:              30.34%       Indels:        26
DB:                       10           Gaps:          2

US-09-900-448-2 (1-391) x US-09-918-995-32820 (1-491)

Qy        120 ProProGluLysLysGluLysGlyTyrProLysLeuLeuGlnAspGluPheProGlyIle 139
              ||||||                  ||||||:::   ::::::|||   |||
Db         92 CCTCCCAGG---------------TACCCGCGGATGTCCGAGACTACTTCATGCCCTGC 136

Qy        140 ProSerProLeuAspAlaAlaValGluCysHisArgGlyGluCysGlnAlaGluGlyVal 159
              |||
Db        137 CCTGGC------------------------------------------------------ 142

Qy        160 LeuPhePheGlnGlyHisGlyHisArgAsnGlyThrGlyHisGlyAsnSerThrHisHis 179
                       :::||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ---------AGAGGCCATGGACACAGGAATGGACTGGCCATGGGAACAGTACCCACCAT 193

Qy        180 GlyProGluTyrMetArgCysSerProHisLeuValLeuSerAlaLeuThrSerAspAsn 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GGCCCTGAGTATATGCGCTGTAGCCCACATCTAGTCTTGTCCGCACTGACGTCTGACAAC 253

Qy        200 HisGlyAlaThrTyrAlaPheSerGlyThrHisTyrTrpArgLeuAspThrSerArgAsp 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 CATGGTGCCACCTATGCCTTCAGTGGGACCCACTACTGGCGTCTGGACACCAGCCGGGAT 313

Qy        220 GlyTrpHisSerTrpProIleAlaHisGlnTrpProGlnGlyProSerAlaValAspAla 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 GGCTGGCATAGCTGGCCCATTGCTCATCAGTGGCCCCAGGGTCCTTCAGCAGTGGATGCT 373

Qy        240 AlaPheSerTrpGluGluLysLeuTyrLeuValGlnGlyThrGlnValTyrValPheLeu 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 GCCTTTTCCTGGGAAGAAAAACTCTATCTGGTCCAGGGCACCCAGGTATATGTCTTCCTG 433

Qy        260 ThrLysGlyGlyTyrThrLeuValSerGlyTyrProLysArgLeuGluLysGluVal 278
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 ACAAAGGGAGGCTATACCCTAGTAAGCGGTTATCCGAAGCGGCTGGAGAAGGAAGTC 490

RESULT 13
US-09-960-352-10323
; Sequence 10323, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 10323
;   LENGTH: 420
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 44-LIB34-041-Q1-E1-C8
US-09-960-352-10323

Alignment Scores:
Pred. No.:                4.73e-56     Length:        420
Score:                    593.00       Matches:       106
Percent Similarity:       85.00%       Conservative:  13
Best Local Similarity:    75.71%       Mismatches:    21
Query Match:              27.14%       Indels:        0
DB:                       9            Gaps:          0

US-09-900-448-2 (1-391) x US-09-960-352-10323 (1-420)

Qy        217 SerArgAspGlyTrpHisSerTrpProIleAlaHisGlnTrpProGlnGlyProSerAla 236
              ||||||||||||||||||||||||   |||   |||   ||||||||||||||||||
Db          1 AGCCGGGACGGGTGGCACAGCTGGCTCATTGAGCATCTGTGGCCCCAAGGTCCCTCAACA 60

Qy        237 ValAspAlaAlaPheSerTrpGluGluLysLeuTyrLeuValGlnGlyThrGlnValTyr 256
              |||||||||||||||   |||::::::||||||||||||:::||||||||||||||||||
Db         61 GTGGATGCTGCCTTTCTCTGGGATAAAAAGCTCTACCTCATCCAGGGTACCCAGGTATAT 120

Qy        257 ValPheLeuThrLysGlyGlyTyrThrLeuValSerGlyTyrProLysArgLeuGluLys 276
              :::|||||||||:::   |||||||||||||||      |||||||||:::|||||||||
Db        121 ATCTTCCTGACAAGGGCAGGCTACACTCTCGTAAAAGATTATCCAAAGCAGCTGGAGAAG 180

Qy        277 GluValGlyThrProHisGlyIleIleLeuAspSerValAspAlaAlaPheIleCysPro 296
              |||   |||:::|||   |||:::   |||   ||||||||||||||||||   ||||||
Db        181 GAATTTGGGAGCCCTGATGGGGTCTGCCTTCATTCTGTGGATGCAGCCTTTACCTGTCCT 240

Qy        297 GlySerSerArgLeuHisIleMetAlaGlyArgArgLeuTrpTrpLeuAspLeuLysSer 316
              |||||||||:::|||:::|||||||||   ::::::||||||   |||||||||
Db        241 GGATCTTCTCAGCTCTACATCATGGCACGCCAGAAGCTGTGGAGGCTGGACCTGAACTTA 300

Qy        317 GlyAlaGlnAlaThrTrpThrGluLeuProTrpProHisGluLysValAspGlyAlaLeu 336
              |||||||||||||||||||||||||||||||||   |||   ||||||||||||||||||
Db        301 GGAGCTCAAGCCACGTGGACAGAGCTTCCTTGGCTCCATACGAAAGTCGATGGGGCCCTG 360

Qy        337 CysMetGluLysSerLeuGlyProAsnSerCysSerAlaAsnGlyProGlyLeuTyrLeu 356
              |||   ||||||||||||||||||:::||||||||||||||||||   ||||||||||||
Db        361 TGTACAGAGAAGTCTCTGGCCCCCACTCGTGTTCTGCCAATGGTCGGGGCTTGTACCTC 420

RESULT 14
US-09-918-995-7738
; Sequence 7738, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7738
;   LENGTH: 384
;   TYPE: DNA
;   ORGANISM: Homo sapiens
```

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US-09-918-995-7738

Alignment Scores:
Pred. No.:              1.24e-51      Length:         384
Score:                  552.50        Matches:        106
Percent Similarity:     86.18%        Conservative:   0
Best Local Similarity:  86.18%        Mismatches:     1
Query Match:            25.29%        Indels:         17
DB:                     10            Gaps:           1

US-09-900-448-2 (1-391) x US-09-918-995-7738 (1-384)

Qy           1 MetAlaArgValLeuGlyAlaProValAlaLeuGlyLeuTrpSerLeuCysTrpSerLeu 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          17 ATGGCTAGGGTACTGGGAGCACCCGTTGCACTGGGGTTGTGGAGCCTATGCTGGTCTCTG 76

Qy          21 AlaIleAlaThrProLeuProProThr--------------------------------- 29
               ||||||||||||||||||||||||
Db          77 GCCATTGCCACCCCTCTTCCTCCGTG-AGTAAAGCTGGGACTAGAAGCGAAGGATTGAGT 135

Qy          30 ---------------SerAlaHisGlyAsnValAlaGluGlyGluThrLysProAspPro 44
                              |||||||||||||||||||||||||||||||||||||||||||||
Db         136 TCTGGGCTAGGGACTAGTGCCCATGGGAATGTTGCTGAAGGCGAGACCAAGCCAGACCCA 195

Qy          45 AspValThrGluArgCysSerAspGlyTrpSerPheAspAlaThrThrLeuAspAspAsn 64
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         196 GACGTGACTGAACGCTGCTCAGATGGCTGGAGCTTTGATGCTACCACCCTGGATGACAAT 255

Qy          65 GlyThrMetLeuPhePheLysGlyGluPheValTrpLysSerHisLysTrpAspArgGlu 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         256 GGAACCATGCTGTTTTTTAAAGGGGAGTTTGTGTGGAAGAGTCACAAATGGGACCGGGAG 315

Qy          85 LeuIleSerGluArgTrpLysAsnPheProSerProValAspAlaAlaPheArgGlnGly 104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         316 TTAATCTCAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAAGGT 375

Qy         105 HisAsnSer 107
               |||||||||
Db         376 CACAACAGT 384

RESULT 15
US-09-918-995-32181
; Sequence 32181, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32181
;   LENGTH: 473
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(473)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32181

Alignment Scores:
Pred. No.:              2.64e-50      Length:         473
Score:                  541.50        Matches:        99
Percent Similarity:     73.83%        Conservative:   11
Best Local Similarity:  66.44%        Mismatches:     16
Query Match:            24.78%        Indels:         23
DB:                     10            Gaps:           2

US-09-900-448-2 (1-391) x US-09-918-995-32181 (1-473)

Qy         109 PheLeuIleLysGlyAspLysValTrpValTyrProProGluLysLysGlu------Lys 126
               :::      :::|||::::::         :::   |||   :::   |||
Db          89 TACTGCTTCCAGGGTAACCAATTCCTGCGCTTCGACCCTGTCAGGGGAGAGGTGCCTCCC 148

Qy         127 GlyTyrProLysLeuLeuGlnAspGluPheProGlyIleProSerProLeuAspAlaAla 146
                  ||||||:::   ::::::|||   |||         |||
Db         149 AGGTACCCGCGGGATGTCCGAGACTACTTCATGCCCTGCCCTGGC--------------- 193

Qy         147 ValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeuPhePheGlnGlyHisGly 166
                                                               :::|||||||||
Db         194 ------------------------------------------------AGAGGCCATGGA 205

Qy         167 HisArgAsnGlyThrGlyHisGlyAsnSerThrHisHisGlyProGluTyrMetArgCys 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         206 CACAGGAATGGACTGGCCATGGGAACAGTACCCACCATGGCCCTGAGTATATGCGCTGT 265

Qy         187 SerProHisLeuValLeuSerAlaLeuThrSerAspAsnHisGlyAlaThrTyrAlaPhe 206
               :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         266 AACCCACATCTAGTCTTGTCTGCACTGACGTCTGACAACCATGGTGCCACCTATGCCTTC 325

Qy         207 SerGlyThrHisTyrTrpArgLeuAspThrSerArgAspGlyTrpHisSerTrpProIle 226
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         326 AGTGGGACCCACTACTGGCGTCTGGACACCAGCCGGGATGGCTGGCATAGCTGGCCCATT 385

Qy         227 AlaHisGlnTrpProGlnGlyProSerAlaValAspAlaAlaPheSerTrpGluGluLys 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         386 GCTCATCAGTGGCCCCAGGGTCCTTCAGCAGTGGATGCTGCCTTTTCCTGGGAAGAAAAA 445

Qy         247 LeuTyrLeuValGlnGlyThrGlnVal 255
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Db         446 CTCTATCTGGTCCAGGGCACCCAGGTA 472


Search completed: June  8, 2004, 07:23:56
Job time : 545 secs
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                    GenCore version 5.1.6
             Copyright (c) 1993 - 2004  Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:         June  8, 2004, 02:37:18 ; Search time 95 Seconds
                                           (without alignments)
                                           2284.061 Million cell updates/sec

Title:          US-09-900-448-2
Perfect score:  2185
Sequence:       1 MARVLGAPVALGLWSLCWSL.........NAAKALPQPQNVTSLLGCTH 391

Scoring table:  BLOSUM62
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                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters:      1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US09900448/runat_07062004_094658_20469/app_query.fasta_1.583
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09900448_@CGN_1_1_56_@runat_07062004_094658_20469 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      Issued_Patents_NA:*
                1:  /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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                5:  /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                6:  /cgn2_6/ptodata/2/ina/backfiles1.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                  SUMMARIES
                %
Result          Query
  No.   Score   Match Length DB  ID                      Description
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   1    202.5    9.3   1410  3  US-08-068-392-1          Sequence 1, Appli
   2    202.5    9.3   1410  3  US-08-396-988-1          Sequence 1, Appli
   3    200.5    9.2   3530  3  US-08-704-711A-10        Sequence 10, Appl
   4    200.5    9.2   3530  4  US-09-521-220-10         Sequence 10, Appl
   5    187.5    8.6   2260  1  US-07-794-393-3          Sequence 3, Appli
   6    187.5    8.6   2260  1  US-08-001-711-3          Sequence 3, Appli
   7      187    8.6   1717  1  US-08-229-515A-12        Sequence 12, Appl
   8      187    8.6   1717  1  US-08-645-865-12         Sequence 12, Appl
   9      185    8.5   3807  2  US-08-816-755-1          Sequence 1, Appli
  10      185    8.5   3807  3  US-09-090-673-1          Sequence 1, Appli
  11    183.5    8.4   2223  1  US-09-178-002-3          Sequence 3, Appli
  12    183.5    8.4   2223  4  US-09-023-655-1040       Sequence 1040, Ap
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  13    183.5    8.4   2247  4  US-09-023-655-1410       Sequence 1410, Ap
  14    183.5    8.4   2256  1  US-07-794-393-1          Sequence 1, Appli
  15    183.5    8.4   2256  1  US-08-001-711-1          Sequence 1, Appli
  16    183.5    8.4   2314  1  US-09-178-002-1          Sequence 1, Appli
  17    181.5    8.3   1970  4  US-09-023-655-1264       Sequence 1264, Ap
  18    181.5    8.3   1981  4  US-09-484-970B-62        Sequence 62, Appl
  19      177    8.1   1160  1  US-07-780-973-15         Sequence 15, Appl
  20      177    8.1   1434  4  US-09-023-655-1174       Sequence 1174, Ap
  21      177    8.1   1801  4  US-09-023-655-1374       Sequence 1374, Ap
  22      176    8.1   1521  4  US-08-994-689C-18        Sequence 18, Appl
  23      176    8.1   2792  4  US-08-994-689C-8         Sequence 8, Appli
  24      174    8.0   1923  3  US-09-294-841-1          Sequence 1, Appli
  25    167.5    7.7   1233  4  US-09-171-545-9          Sequence 9, Appli
  26    167.5    7.7   1248  4  US-09-171-545-10         Sequence 10, Appl
  27    167.5    7.7   1524  4  US-09-171-545-7          Sequence 7, Appli
  28    167.5    7.7   2264  4  US-09-171-545-22         Sequence 22, Appl
  29    160.5    7.3   3403  3  US-08-448-489-2          Sequence 2, Appli
  30    157.5    7.2   2049  4  US-09-171-545-23         Sequence 23, Appl
  31      156    7.1   2275  4  US-09-391-104-1          Sequence 1, Appli
  32    155.5    7.1   3437  3  US-08-704-711A-9         Sequence 9, Appli
  33    155.5    7.1   3437  4  US-09-521-220-9          Sequence 9, Appli
  34    155.5    7.1   3456  3  US-08-704-711A-8         Sequence 8, Appli
  35    155.5    7.1   3456  4  US-09-521-220-8          Sequence 8, Appli
  36      154    7.0   1257  4  US-09-171-545-11         Sequence 11, Appl
  37      154    7.0   1272  4  US-09-171-545-12         Sequence 12, Appl
  38      154    7.0   1551  4  US-09-171-545-8          Sequence 8, Appli
  39      154    7.0   3813  4  US-07-757-022B-43        Sequence 43, Appl
  40      154    7.0   3936  4  US-07-757-022B-41        Sequence 41, Appl
  41      154    7.0   3942  4  US-07-757-022B-141       Sequence 141, App
  42      154    7.0   3945  4  US-07-757-022B-49        Sequence 49, Appl
  43      154    7.0   3963  4  US-07-757-022B-45        Sequence 45, Appl
  44      154    7.0   3963  4  US-07-757-022B-59        Sequence 59, Appl
  45      154    7.0   4065  4  US-07-757-022B-47        Sequence 47, Appl

                                  ALIGNMENTS

RESULT 1
US-08-068-392-1
; Sequence 1, Application US/08068392
; Patent No. 6150152
;  GENERAL INFORMATION:
;    APPLICANT:  Shapiro, Steven M.
;    TITLE OF INVENTION:  Human Macrophage Metalloproteinase
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scott J. Meyer, Monsanto Co., A3SM
;      STREET:  800 N. Lindbergh Blvd.
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63167
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/068,392
;      FILING DATE:  19930528
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyer, Scott J.
;      REGISTRATION NUMBER:  25275
;      REFERENCE/DOCKET NUMBER:  07-24(12406)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)694-3117
;      TELEFAX:  (314)694-5435
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1410 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1410
US-08-068-392-1

Alignment Scores:
Pred. No.:              1.72e-10      Length:        1410
Score:                  202.50        Matches:       66
Percent Similarity:     36.78%        Conservative:  23
Best Local Similarity:  27.27%        Mismatches:    90
Query Match:            9.27%         Indels:        63
DB:                     3             Gaps:          10

US-09-900-448-2 (1-391) x US-08-068-392-1 (1-1410)

Qy         30 SerAlaHisGlyAsnValAlaGluGlyGluThrLysProAspProAspValThrGlu--- 48
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Db        778 TCCCTGTATGGAGACCCAAAAGAGAACCAACGCTTGCCAAATCCTGACAATTCAGAACCA 837

Qy         49 ---ArgCysSerAspGlyTrpSerPheAspAlaThrThrLeuAspAspAsnGlyThrMet 67
                    |||            ||||||||||||   |||         |||      :::
Db        838 GCTCTCTGTGACCCCAATTTGAGTTTTGATGCTGTCACTACCGTGGGAAAT---AAGATC 894

Qy         68 LeuPhePheLysGlyGluPheValTrp------------LysSerHisLysTrpAspArg 83
                 |||||||||      |||   |||            :::      |||
Db        895 TTTTTCTTCAAAGACAGGTTCTTCTGGCTGAAGGTTTCTGAGAGACCAAAGACCAGTGTT 954

Qy         84 GluLeuIleSerGluArgTrpLysAsnPheProSerProValAspAlaAlaPheArg--- 102
                 |||||||||      |||         ||||||   ::::::||||||:::
Db        955 AATTTAATTTCTTCCTTATGGCCAACCTTGCCATCTGGCATTGAAGCTGCTTATGAAATT 1014

Qy        103 GlnGlyHisAsnSerValPheLeuIleLysGlyAspLysValTrpValTyrProProGlu 122
              :::      |||   |||||||||   |||   ||||||   |||:::
Db       1015 GAAGCCAGAAATCAAGTTTTTCTTTTTAAAGATGACAAATACTGGTTAATTAGCAATTTA 1074

Qy        123 LysLysGluLysGlyTyrProLysLeuLeuGlnAsp---GluPheProGlyIleProSer 141
              :::   |||      |||||||||   :::            ||||||
Db       1075 AGACCAGAGCCAAATTATCCCAAGAGCATACATTCTTTTGGTTTTCCTAACTTTGTGAAA 1134

Qy        142 ProLeuAspAlaAlaValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeuPhe 161
                 :::||||||||||||
Db       1135 AAAATTGATGCAGCTGTT------------------------------------------ 1152

Qy        162 PheGlnGlyHisGlyHisArgAsnGlyThrGlyHisGlyAsnSerThrHisHisGlyPro 181
                                                                       |||
Db       1153 ---------------------------------------------------TTTAACCCA 1161

Qy        182 GluTyrMetArgCysSerProHisLeuValLeuSerAlaLeuThrSerAspAsnHisGly 201
                 :::   |||
Db       1162 CGTTTTTATAGG------------------------------------------------ 1173

Qy        202 AlaThrTyrAlaPheSerGlyThrHisTyrTrpArgLeuAspThrSerArgAsp------ 219
                 ||||||   |||            |||||||||   |||      |||
Db       1174 ---ACCTACTTCTTTGTAGATAACCAGTATTGGAGGTATGATGAAAGGAGACAGATGATG 1230

Qy        220 ------GlyTrpHisSerTrpProIleAlaHisGlnTrpProGlnGlyProSerAlaVal 237
                    |||:::                  :::            ||||||      :::
Db       1231 GACCCTGGTTATCCCAAACTGATTACCAAGAACTTCCAAGGAATCGGGCCTAAA---ATT 1287

Qy        238 AspAlaAlaPheSerTrpGluGluLys---LeuTyrLeuValGlnGlyThrGlnValTyr 256
              ||||||   |||      :::   |||      |||      ||||||:::      :::
Db       1288 GATGCAGTCTTCTATTCTAAAAACAAATACTACTATTTCTTCCAAGGATCTAACCAATTT 1347

Qy        257 ValPhe 258
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Db       1348 GAATAT 1353

RESULT 2
US-08-396-988-1
; Sequence 1, Application US/08396988
; Patent No. 6204043
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; GENERAL INFORMATION:
;   APPLICANT:  Shapiro, Steven M.
;   TITLE OF INVENTION:  Human Macrophage Metalloproteinase
;   NUMBER OF SEQUENCES:  3
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Scott J. Meyer, Monsanto Co., A3SM
;     STREET:  800 N. Lindbergh Blvd.
;     CITY:  St. Louis
;     STATE:  Missouri
;     COUNTRY:  USA
;     ZIP:  63167
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/396,988
;     FILING DATE:  01-MAR-1995
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/068,392
;     FILING DATE:  28-MAY-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Meyer, Scott J.
;     REGISTRATION NUMBER:  25275
;     REFERENCE/DOCKET NUMBER:  07-24(12406)A
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (314)694-3117
;     TELEFAX:  (314)694-5435
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1410 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1410
US-08-396-988-1

Alignment Scores:
Pred. No.:              1.72e-10      Length:        1410
Score:                  202.50        Matches:       66
Percent Similarity:     36.78%        Conservative:  23
Best Local Similarity:  27.27%        Mismatches:    90
Query Match:            9.27%         Indels:        63
DB:                     3             Gaps:          10

US-09-900-448-2 (1-391) x US-08-396-988-1 (1-1410)

Qy         30 SerAlaHisGlyAsnValAlaGluGlyGluThrLysProAspProAspValThrGlu--- 48
              |||   :::|||:::      |||   :::      |||:::||||||   :::|||
Db        778 TCCCTGTATGGAGACCCAAAAGAGAACCAACGCTTGCCAAATCCTGACAATTCAGAACCA 837

Qy         49 ---ArgCysSerAspGlyTrpSerPheAspAlaThrThrLeuAspAspAsnGlyThrMet 67
                    |||            ||||||||||||   |||         |||      :::
Db        838 GCTCTCTGTGACCCCAATTTGAGTTTTGATGCTGTCACTACCGTGGGAAAT---AAGATC 894

Qy         68 LeuPhePheLysGlyGluPheValTrp------------LysSerHisLysTrpAspArg 83
                 |||||||||      |||   |||            :::      |||
Db        895 TTTTTCTTCAAAGACAGGTTCTTCTGGCTGAAGGTTTCTGAGAGACCAAAGACCAGTGTT 954

Qy         84 GluLeuIleSerGluArgTrpLysAsnPheProSerProValAspAlaAlaPheArg--- 102
                 |||||||||      |||         ||||||   ::::::||||||:::
Db        955 AATTTAATTTCTTCCTTATGGCCAACCTTGCCATCTGGCATTGAAGCTGCTTATGAAATT 1014

Qy        103 GlnGlyHisAsnSerValPheLeuIleLysGlyAspLysValTrpValTyrProProGlu 122
              :::      |||   |||||||||   |||   ||||||   |||:::
Db       1015 GAAGCCAGAAATCAAGTTTTTCTTTTTAAAGATGACAAATACTGGTTAATTAGCAATTTA 1074

Qy        123 LysLysGluLysGlyTyrProLysLeuLeuGlnAsp---GluPheProGlyIleProSer 141
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              :::   |||      |||||||||   :::            ||||||
Db       1075 AGACCAGAGCCAAATTATCCCAAGAGCATACATTCTTTTGGTTTTCCTAACTTTGTGAAA 1134

Qy        142 ProLeuAspAlaAlaValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeuPhe 161
                 :::||||||||||||
Db       1135 AAAATTGATGCAGCTGTT------------------------------------------ 1152

Qy        162 PheGlnGlyHisGlyHisArgAsnGlyThrGlyHisGlyAsnSerThrHisHisGlyPro 181
                                                                       |||
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Qy        182 GluTyrMetArgCysSerProHisLeuValLeuSerAlaLeuThrSerAspAsnHisGly 201
                 :::   |||
Db       1162 CGTTTTTATAGG------------------------------------------------ 1173

Qy        202 AlaThrTyrAlaPheSerGlyThrHisTyrTrpArgLeuAspThrSerArgAsp------ 219
                 ||||||   |||            |||||||||   |||      |||
Db       1174 ---ACCTACTTCTTTGTAGATAACCAGTATTGGAGGTATGATGAAAGGAGACAGATGATG 1230

Qy        220 ------GlyTrpHisSerTrpProIleAlaHisGlnTrpProGlnGlyProSerAlaVal 237
                    |||:::                  :::            ||||||      :::
Db       1231 GACCCTGGTTATCCCAAACTGATTACCAAGAACTTCCAAGGAATCGGGCCTAAA---ATT 1287

Qy        238 AspAlaAlaPheSerTrpGluGluLys---LeuTyrLeuValGlnGlyThrGlnValTyr 256
              ||||||   |||      :::   |||      |||      ||||||:::      :::
Db       1288 GATGCAGTCTTCTATTCTAAAAACAAATACTACTATTTCTTCCAAGGATCTAACCAATTT 1347

Qy        257 ValPhe 258
                 :::
Db       1348 GAATAT 1353
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RESULT 3
US-08-704-711A-10
; Sequence 10, Application US/08704711A
; Patent No. 6114159
;  GENERAL INFORMATION:
;    APPLICANT:  WILL, Horst
;    APPLICANT:  HINZMANN, Bernd
;    TITLE OF INVENTION:  DNA SEQUENCES FOR MATRIX
;    TITLE OF INVENTION:  METALLOPROTEASES, THEIR PRODUCTION AND USE
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/704,711A
;      FILING DATE:  20-NOV-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/DE95/00357
;      FILING DATE:  17-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE 4438838.1
;      FILING DATE:  21-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE 4409663.1
;      FILING DATE:  17-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GRANADOS, Patricia D.
;      REGISTRATION NUMBER:  33,683
;      REFERENCE/DOCKET NUMBER:  26083/124
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3530 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-704-711A-10

Alignment Scores:
Pred. No.:              1.03e-09        Length:         3530
Score:                  200.50          Matches:        90
Percent Similarity:     33.33%          Conservative:   37
Best Local Similarity:  23.62%          Mismatches:     141
Query Match:            9.18%           Indels:         113
DB:                     3               Gaps:           18

US-09-900-448-2 (1-391) x US-08-704-711A-10 (1-3530)

Qy         25 ProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGluThrLysProAspPro 44
              |||   ||||||            |||         |||         ||||||   |||
Db       1051 CCCCAGCCACCACCCCCA------GGTGGGAAGCCAGAGCGGCCCCCAAAGCCGGGCCCC 1104

Qy         45 AspValThrGluArgCysSer---------------------------------AspGly 53
                 |||      |||   :::                                 ||||||
Db       1105 CCAGTCCAGCCCCGAGCCACAGAGCGGCCCGACCAGTATGGCCCCAACATCTGCGACGGG 1164

Qy         54 TrpSerPheAspAlaThrThrLeuAspAspAsnGlyThrMetLeuPhePheLysGlyGlu 73
                    ||||||         :::         |||   |||      |||||||||
Db       1165 ---GACTTTGACACAGTGGCCATG---CTTCGCGGGGAGATGTTCGTGTTCAAGGGCCGC 1218

Qy         74 PheValTrpLysSerHisLysTrpAspArgGluLeu------------------IleSer 87
              :::   |||:::      :::   :::|||   |||                  |||
Db       1219 TGGTTCTGGCGAGTC---CGGCACAACCGCGTCCTGGACAACTATCCCATGCCCATCGGG 1275

Qy         88 GluArgTrpLysAsnPheProSerProValAspAlaAlaPheArgGlnGlyHisAsnSer 107
                    |||:::      |||      :::   ||||||:::   :::
Db       1276 CACTTCTGGCGTGGTCTGCCCGGTGACATCAGTGCTGCCTACGAGCGCCAAGACGGTCGT 1335

Qy        108 ValPheLeuIleLysGlyAspLysValTrpValTyrProProGluLysLysGluLysGly 127
                          |||||||||:::   |||::::::               |||   |||
Db       1336 TTTGTCTTTTTCAAAGGTGACCGCTACTGGCTCTTTCGAGAAGCGAACCTGGAGCCCGGC 1395

Qy        128 TyrProLysLeuLeuGlnAspGluPheProGlyIlePro---SerProLeuAspAlaAla 146
              ||||||:::   |||               |||||||||         :::|||   |||
Db       1396 TACCCACAGCCGCTGACCAGCTATGGCCTGGGCATCCCCTATGACCGCATTGACACGGCC 1455

Qy        147 ValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeuPhePheGlnGlyHisGly 166
              :::                                       :::::::::      |||
Db       1456 ATC---------------------------------------TGGTGGGAGCCCACAGGC 1476

Qy        167 His---------------------------------ArgAsnGlyThrGlyHisGly 174
              |||                                             |||      |||
Db       1477 CACACCTTCTTCTTCCAAGAGGACAGGTACTGGCGCTTCAACGAGGAGACACAGCGTGGA 1536

Qy        175 AsnSerThrHisHisGlyPro------------GluTyrMetArgCysSerProHisLeu 190
              :::      :::      |||            :::   :::      ||||||
Db       1537 GACCCTGGGTACCCCAAGCCCATCAGTGTCTGGCAGGGGATCCCTGCCTCCCCTAAA--- 1593

Qy        191 ValLeuSerAlaLeuThrSerAspAsnHisGlyAlaThrTyrAlaPheSerGlyThrHis 210
                       |||      |||::::::         ||||||   :::   ||||||
Db       1594 ------GGGGCCTTCCTGAGCAATGACGCAGCCTACACCTACTTCTACAAGGGCACCAAA 1647

Qy        211 TyrTrpArgLeuAspThrSerArg-AspGlyTrpHis----------------------- 222
              ||||||:::   |||      |||    ||||||
Db       1648 TACTGGAAATTCGACAATGAGCGCCTGCGGATGGAGCCCGGCTACCCCAAGTCCATCCTG 1707

Qy        223 -------SerTrpProIleAlaHisGlnTrpProGlnGlyProSerAlaValAspAlaAl 240
                     ||||||               |||   |||   |||
Db       1708 CGGGACTTCATGGGCTGCCAGGAGCACGTGGAGCCAGGCCCCCGATGGCCCG-------- 1759

Qy        240 aPheSerTrpGluGluLysLeuTyrLeuValGlnGlyThrGlnValTyrValPheLeuTh 260
                  :::|||      :::               |||   |||
Db         1760 ----ACGTGGCCCGGCCGCCCTTCAACCCCCACGGGGGTGCAG----------------- 1798

Qy          260 rLysGlyGlyTyrThrLeuValSerGlyTyrProLysArgLeuGluLysGluValGlyTh 280
                                               |||   |||      :::
Db         1799 ----------------------------AGCCCGGGGCGGACAGCGCAGAGGGCGACGTG 1830

Qy          280 rProHisGlyIleIleLeuAspSerValAspAlaAlaPheIleCysProGlySerSerAr 300
                       |||:::                           :::   |||||||||:::||
Db         1831 GGGGATGGGGATG---------------------GGGACTTTGGGGCCGGGTCAACAAG 1869

Qy          300 gLeuHisIleMetAlaGlyArgArgLeuTrpTrp-LeuAspLeuLysSerGlyAlaGlnA 320
                |               |||         ||||||    |||         |||
Db         1870 G------------ACGGGGGCAGCCGCGTGGTGGTGCAGATGGAGGAGGTGGCACGGACG 1917

Qy          320 laThrTrpThrGluLeuProTrpProHisGluLysValAspGlyAlaLeuCysMetGluL 340
                                             |||:::   |||||||||
Db         1918 GT---------------------------GAACGTGGTGATGGTGCT------------- 1937

Qy          340 ysSerLeuGlyProAsnSerCysSerAlaAsnGlyProGlyLeuTyrLeuIleHisGly 359
                        |||      :::   :::|||      ||||||   :::|||      |||
Db         1938 --------GGTGCCACTGCTGCTGCTGCTCTGCGTCCTGGGCCTCACCTACGCGCTGGT 1988

RESULT 4
US-09-521-220-10
; Sequence 10, Application US/09521220
; Patent No. 6399348
;  GENERAL INFORMATION:
;       APPLICANT: WILL, Horst
;                  HINZMANN, Bernd
;       TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
;                           METALLOPROTEASES, THEIR PRODUCTION AND USE
;       NUMBER OF SEQUENCES: 22
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/521,220
;            FILING DATE: 08-Mar-2000
;            CLASSIFICATION: <Unknown>
;                            21-OCT-1994
;                            17-MAR-1994
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/704,711
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: DE 4438838.1
;            FILING DATE: 21-OCT-1994
;            APPLICATION NUMBER: DE 4409663.1
;            FILING DATE: 17-MAR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: GRANADOS, Patricia D.
;            REGISTRATION NUMBER: 33,683
;            REFERENCE/DOCKET NUMBER: 26083/124
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 10:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 3530 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-521-220-10
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Alignment Scores:
Pred. No.:                 1.03e-09        Length:          3530
Score:                     200.50          Matches:         90
Percent Similarity:        33.33%          Conservative:    37
Best Local Similarity:     23.62%          Mismatches:      141
Query Match:               9.18%           Indels:          113
DB:                        4               Gaps:            18

US-09-900-448-2 (1-391) x US-09-521-220-10 (1-3530)

Qy           25 ProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGluThrLysProAspPro 44
                |||   ||||||            |||         |||         ||||||   |||
Db         1051 CCCCAGCCACCACCCCCA------GGTGGGAAGCCAGAGCGGCCCCCAAAGCCGGGCCCC 1104

Qy           45 AspValThrGluArgCysSer---------------------------------AspGly 53
                   |||      |||   :::                                 ||||||
Db         1105 CCAGTCCAGCCCCGAGCCACAGAGCGGCCCGACCAGTATGGCCCCAACATCTGCGACGGG 1164

Qy           54 TrpSerPheAspAlaThrThrLeuAspAspAsnGlyThrMetLeuPhePheLysGlyGlu 73
                      ||||||         :::         |||   |||      |||||||||
Db         1165 ---GACTTTGACACAGTGGCCATG---CTTCGCGGGGAGATGTTCGTGTTCAAGGGCCGC 1218

Qy           74 PheValTrpLysSerHisLysTrpAspArgGluLeu------------------IleSer 87
                :::   |||:::      :::   :::|||   |||                  |||
Db         1219 TGGTTCTGGCGAGTC---CGGCACAACCGCGTCCTGGACAACTATCCCATGCCCATCGGG 1275

Qy           88 GluArgTrpLysAsnPheProSerProValAspAlaAlaPheArgGlnGlyHisAsnSer 107
                      |||:::      |||      :::   ||||||:::   :::
Db         1276 CACTTCTGGCGTGGTCTGCCCGGTGACATCAGTGCTGCCTACGAGCGCCAAGACGGTCGT 1335

Qy          108 ValPheLeuIleLysGlyAspLysValTrpValTyrProProGluLysLysGluLysGly 127
                            |||||||||:::   |||::::::               |||   |||
Db         1336 TTTGTCTTTTTCAAAGGTGACCGCTACTGGCTCTTTCGAGAAGCGAACCTGGAGCCCGGC 1395

Qy          128 TyrProLysLeuLeuGlnAspGluPheProGlyIlePro---SerProLeuAspAlaAla 146
                ||||||:::   |||               |||||||||         :::|||   |||
Db         1396 TACCCACAGCCGCTGACCAGCTATGGCCTGGGCATCCCCTATGACCGCATTGACACGGCC 1455

Qy          147 ValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeuPhePheGlnGlyHisGly 166
                :::                                       :::::::::      |||
Db         1456 ATC---------------------------------------TGGTGGGAGCCCACAGGC 1476

Qy          167 His------------------------------------ArgAsnGlyThrGlyHisGly 174
                |||                                             |||      |||
Db         1477 CACACCTTCTTCTTCCAAGAGGACAGGTACTGGCGCTTCAACGAGGAGACACAGCGTGGA 1536

Qy          175 AsnSerThrHisHisGlyPro------------GluTyrMetArgCysSerProHisLeu 190
                :::      :::      |||            :::   :::      ||||||
Db         1537 GACCCTGGGTACCCCAAGCCCATCAGTGTCTGGCAGGGGATCCCTGCCTCCCCTAAA--- 1593

Qy          191 ValLeuSerAlaLeuThrSerAspAsnHisGlyAlaThrTyrAlaPheSerGlyThrHis 210
                         |||      |||::::::         ||||||   :::   ||||||
Db         1594 ------GGGGCCTTCCTGAGCAATGACGCAGCCTACACCTACTTCTACAAGGGCACCAAA 1647

Qy          211 TyrTrpArgLeuAspThrSerArg-AspGlyTrpHis----------------------- 222
                ||||||:::   |||      |||    ||||||
Db         1648 TACTGGAAATTCGACAATGAGCGCCTGCGGATGGAGCCCGGCTACCCCAAGTCCATCCTG 1707

Qy          223 -------SerTrpProIleAlaHisGlnTrpProGlnGlyProSerAlaValAspAlaAl 240
                       ||||||               |||   |||   |||
Db         1708 CGGGACTTCATGGGCTGCCAGGAGCACGTGGAGCCAGGCCCCCGATGGCCCG-------- 1759

Qy          240 aPheSerTrpGluGluLysLeuTyrLeuValGlnGlyThrGlnValTyrValPheLeuTh 260
                    :::|||      :::               |||   |||
Db         1760 ----ACGTGGCCCGGCCGCCCTTCAACCCCCACGGGGGTGCAG----------------- 1798

Qy          260 rLysGlyGlyTyrThrLeuValSerGlyTyrProLysArgLeuGluLysGluValGlyTh 280
                                               |||   |||      :::
Db         1799 ----------------------------AGCCCGGGGCGGACAGCGCAGAGGGCGACGTG 1830

Qy          280 rProHisGlyIleIleLeuAspSerValAspAlaAlaPheIleCysProGlySerSerAr 300
                       |||:::                           :::   |||||||||:::||
Db      1831 GGGATGGGGATG----------------------GGGACTTTGGGGCCGGGGTCAACAAG 1869

Qy       300 gLeuHisIleMetAlaGlyArgArgLeuTrpTrp-LeuAspLeuLysSerGlyAlaGlnA 320
             |               |||         ||||||    |||         |||
Db      1870 G------------ACGGGGGCAGCCGCGTGGTGGTGCAGATGGAGGAGGTGGCACGGACG 1917

Qy       320 laThrTrpThrGluLeuProTrpProHisGluLysValAspGlyAlaLeuCysMetGluL 340
                                          |||:::   |||||||||
Db      1918 GT---------------------------GAACGTGGTGATGGTGCT------------- 1937

Qy       340 ysSerLeuGlyProAsnSerCysSerAlaAsnGlyProGlyLeuTyrLeuIleHisGly 359
                     |||      :::   :::|||      ||||||   :::|||      |||
Db      1938 --------GGTGCCACTGCTGCTGCTGCTCTGCGTCCTGGGCCTCACCTACGCGCTGGT 1988

RESULT 5
US-07-794-393-3
; Sequence 3, Application US/07794393
; Patent No. 5236844
;  GENERAL INFORMATION:
;    APPLICANT:  CHAMBON, PIERRE
;    APPLICANT:  BASSET, PAUL
;    APPLICANT:  BELLOCQ, JEAN-PIERRE
;    TITLE OF INVENTION:  ANALYTICAL MARKERS FOR MALIGNANT BREAST
;    TITLE OF INVENTION:  CANCER
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1225 Connecticut Ave. NW Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/794,393
;      FILING DATE:  19911121
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9025326.1
;      FILING DATE:  21-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GOLDSTEIN, JORGE A
;      REGISTRATION NUMBER:  29,021
;      REFERENCE/DOCKET NUMBER:  1383.0040000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 466-0800
;      TELEFAX:  (202) 833-8716
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2260 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  11..1486
US-07-794-393-3

Alignment Scores:
Pred. No.:               1.03e-08      Length:          2260
Score:                   187.50        Matches:         90
Percent Similarity:      32.98%        Conservative:    34
Best Local Similarity:   23.94%        Mismatches:      126
Query Match:             8.58%         Indels:          127
DB:                      1             Gaps:            16

US-09-900-448-2 (1-391) x US-07-794-393-3 (1-2260)
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Qy        24 ThrProLeuProProThrSerAlaHis---------------GlyAsnValAlaGluGly 38
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Db       818 TCCCCCGCCCCAACTTTGAGCTCCCAGGCTGGGACAGATACCAATGAGATTGCACTGCTG 877

Qy        39 GluThrLysProAspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAla 58
             |||   :::      |||||||||   |||                  ||||||||||||
Db       878 GAGCCGGAAACCCCGCCAGATGTCTGTGAGACT---------------TCCTTCGACGCG 922

Qy        59 ThrThrLeuAspAspAsnGlyThrMetLeuPhePheLysGlyGluPheValTrpLysSer 78
                :::            |||   :::   |||||||||      |||||||||:::
Db       923 GTTTCC---ACCATCCGAGGAGAGCTCTTCTTCTTCAAGGCAGGCTTTGTGTGGAGGCTG 979

Qy        79 HisLysTrpAspArgGlu---------------LeuIleSerGluArgTrpLysAsnPhe 93
                            :::               |||   |||      |||:::
Db       980 CGCAGTGGGCGACTGCAGCCCGGGTATCCTGCTTTGGCCTCTCGGCACTGGCAAGGACTG 1039

Qy        94 ProSerProValAspAlaAlaPheArgGlnGlyHisAsnSerValPheLeuIleLysGly 113
             ||||||||||||||||||||||||                  ::::::      :::|||
Db      1040 CCCAGCCCTGTGGATGCAGCTTTTGAGGATGCCCAGGGCCAGATTTGGTTCTTCCAAGGT 1099

Qy       114 AspLysValTrpValTyrProProGluLysLysGluLysGlyTyrProLysLeuLeuGln 133
                :::   |||||||||      ||||||         |||         |||   :::
Db      1100 GCTCAGTACTGGGTATATGATGGTGAGAAGCCAGTCCTAGGCCCTGCACCACTCTCCAAG 1159

Qy       134 AspGluPheProGlyIleProSerProLeuAspAlaAlaValGluCysHisArgGlyGlu 153
                         |||      ||||||:::   ||||||:::
Db      1160 CTGGGCCTGCAAGGG------TCCCCAGTTCATGCCGCCTTGGTC--------------- 1198

Qy       154 CysGlnAlaGluGlyValLeuPhePheGlnGlyHisGlyHisArgAsnGlyThrGlyHis 173

Db      1198 ------------------------------------------------------------ 1198

Qy       174 GlyAsnSerThrHisHisGlyProGluTyrMetArgCysSerProHisLeuValLeuSer 193
                               |||||||||
Db      1199 ---------------TGGGGTCCTGAG--------------------------------- 1210

Qy       194 AlaLeuThrSerAspAsnHisGlyAlaThrTyrAlaPheSerGlyThrHisTyrTrpArg 213
                                           |||   |||   |||      |||||||||
Db      1211 ------------------AAGAACAAGATCTACTTCTTCCGAGGTGGAGACTATTGGCGT 1252

Qy       214 LeuAsp------ThrSerArgAspGlyTrpHisSerTrpProIleAlaHis-GlnTrpPr 231
                         |||   |||   |||            |||      |||    |||
Db      1253 TTCCACCCCAGAACCCAGCGAGT-GGACAATCCCGTGCCCCGGCGCTCCACTGACTGGCG 1311

Qy       231 oGlnGlyProSerAlaValAspAlaAlaPheSerTrpGluGluLysLeuTyrLeuValGl 251
                    ||||||   :::||||||||||||                           ||
Db      1312 AGGGGTACCTTCTGAGATTGATGCTGCCTTC---------------------------CA 1344

Qy       251 nGlyThrGlnValTyrValPheLeuThrLysGlyGlyTyrThrLeuValSerGlyTyrPr 271
             |      :::   |||   :::      :::   |||:::                  ||
Db      1345 GGATGCTGAGGGCTATGCCTACTTCCTTCGT---GGCCATCTCTACTGGAAGTTTGATCC 1401

Qy       271 oLysArgLeuGluLysGluValGlyThrProHisGlyIleIleLeuAspSerValAspAl 291
             |   :::::::::         |||   |||      :::      |||      |||
Db      1402 CGTGAAGGTGAAGGTCCTAGAAGGCTTTCCTCGCCCCGTAGGTCCTGACTTCTTTGACTG 1461

Qy       291 aAla------------------------------PheIleCys----------------- 295
              |||                              |||   |||
Db      1462 TGCTGAGCCTGCCAATACTTTCCGCTGACAACACTTTGGATGCATTCAGGGGTACTGACT 1521

Qy       296 ----ProGlySerSerArgLeuHisIleMetAlaGlyArgArgLeuTrpTrpLeuAspLe 314
                 ||||||            |||:::         :::         ||||||   ||
Db      1522 CCTGCCAGGGCACTTAGAT---CATGTAAGAGACCCACAGCCATATCTGTGGCTCTGGCT 1578

Qy       314 uLysSerGlyAlaGlnAlaThrTrpThrGluLeuProTrpProHisGluLysValAspGl 334
             |::::::                              |||      :::
Db      1579 TCAGGCA------------------------------TGGGACAGACAG----------- 1597

Qy       334 yAlaLeuCysMetGluLysSerLeuGly-------------------------------- 343
                 ||||||:::   :::   :::|||
Db      1598 -GGCCTATGTCTCCTCAGGGGAGTGGGTTGGGGTGCAGCCACTGTTTGTAGGAACGACCA 1656

Qy       344 ----------------ProAsnSerCysSerAlaAsnGlyProGly 353
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Db        1657 TGCTGTCATGTCACCTGCCAACAATTGTCTCAGACTAGGCAAAGGC 1702

RESULT 6
US-08-001-711-3
; Sequence 3, Application US/08001711
; Patent No. 5484726
;  GENERAL INFORMATION:
;    APPLICANT:  BASSET, PAUL
;    APPLICANT:  BELLOCQ, JEAN-PIERRE
;    APPLICANT:  CHAMBON, PIERRE
;    TITLE OF INVENTION:  ANALYTICAL MARKERS FOR MALIGNANT BREAST
;    TITLE OF INVENTION:  CANCER
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1225 Connecticut Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/001,711
;      FILING DATE:  19930107
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/794,393
;      FILING DATE:  11-NOV-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9025626.1
;      FILING DATE:  21-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLMAN, ROBERT A
;      REGISTRATION NUMBER:  36,217
;      REFERENCE/DOCKET NUMBER:  1383.0040001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)466-0800
;      TELEFAX:  (202)833-8716
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2260 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  11..1486
US-08-001-711-3

Alignment Scores:
Pred. No.:              1.03e-08       Length:        2260
Score:                  187.50         Matches:       90
Percent Similarity:     32.98%         Conservative:  34
Best Local Similarity:  23.94%         Mismatches:    126
Query Match:            8.58%          Indels:        127
DB:                     1              Gaps:          16

US-09-900-448-2 (1-391) x US-08-001-711-3 (1-2260)

Qy          24 ThrProLeuProProThrSerAlaHis---------------GlyAsnValAlaGluGly 38
               :::|||   |||      |||:::                        :::|||
Db         818 TCCCCCGCCCCAACTTTGAGCTCCCAGGCTGGGACAGATACCAATGAGATTGCACTGCTG 877

Qy          39 GluThrLysProAspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAla 58
               |||   :::      |||||||||   |||                  ||||||||||||
Db         878 GAGCCGGAAACCCCGCCAGATGTCTGTGAGACT---------------TCCTTCGACGCG 922

Qy          59 ThrThrLeuAspAspAsnGlyThrMetLeuPhePheLysGlyGluPheValTrpLysSer 78
                  :::            |||   :::   |||||||||      |||||||||:::
Db         923 GTTTCC---ACCATCCGAGGAGAGCTCTTCTTCTTCAAGGCAGGCTTTGTGTGGAGGCTG 979

Qy          79 HisLysTrpAspArgGlu---------------LeuIleSerGluArgTrpLysAsnPhe 93
                              :::               |||   |||      |||:::
Db         980 CGCAGTGGGCGACTGCAGCCCGGGTATCCTGCTTTGGCCTCTCGGCACTGGCAAGGACTG 1039

Qy          94 ProSerProValAspAlaAlaPheArgGlnGlyHisAsnSerValPheLeuIleLysGly 113
               ||||||||||||||||||||||||                  ::::::      :::|||
Db        1040 CCCAGCCCTGTGGATGCAGCTTTTGAGGATGCCCAGGGCCAGATTTGGTTCTTCCAAGGT 1099

Qy         114 AspLysValTrpValTyrProProGluLysLysGluLysGlyTyrProLysLeuLeuGln 133
                  :::   |||||||||      ||||||         |||         |||   :::
Db        1100 GCTCAGTACTGGGTATATGATGGTGAGAAGCCAGTCCTAGGCCCTGCACCACTCTCCAAG 1159

Qy         134 AspGluPheProGlyIleProSerProLeuAspAlaAlaValGluCysHisArgGlyGlu 153
                           |||      ||||||:::   ||||||:::
Db        1160 CTGGGCCTGCAAGGG------TCCCAGTTCATGCCGCCTTGGTC---------------- 1198

Qy         154 CysGlnAlaGluGlyValLeuPhePheGlnGlyHisGlyHisArgAsnGlyThrGlyHis 173

Db        1198 ------------------------------------------------------------ 1198

Qy         174 GlyAsnSerThrHisHisGlyProGluTyrMetArgCysSerProHisLeuValLeuSer 193
                                 |||||||||
Db        1199 ---------------TGGGGTCCTGAG--------------------------------- 1210

Qy         194 AlaLeuThrSerAspAsnHisGlyAlaThrTyrAlaPheSerGlyThrHisTyrTrpArg 213
                                             |||   |||   |||      |||||||||
Db        1211 ------------------AAGAACAAGATCTACTTCTTCCGAGGTGGAGACTATTGGCGT 1252

Qy         214 LeuAsp------ThrSerArgAspGlyTrpHisSerTrpProIleAlaHis-GlnTrpPr 231
                           |||   |||   |||            |||      |||    |||
Db        1253 TTCCACCCCAGAACCCAGCGAGT-GGACAATCCCGTGCCCCGGCGCTCCACTGACTGGCG 1311

Qy         231 oGlnGlyProSerAlaValAspAlaAlaPheSerTrpGluGluLysLeuTyrLeuValGl 251
                      ||||||   :::||||||||||||                           ||
Db        1312 AGGGGTACCTTCTGAGATTGATGCTGCCTTC---------------------------CA 1344

Qy         251 nGlyThrGlnValTyrValPheLeuThrLysGlyGlyTyrThrLeuValSerGlyTyrPr 271
               |      :::   |||   :::      :::   |||:::                  ||
Db        1345 GGATGCTGAGGGCTATGCCTACTTCCTTCGT---GGCCATCTCTACTGGAAGTTTGATCC 1401

Qy         271 oLysArgLeuGluLysGluValGlyThrProHisGlyIleIleLeuAspSerValAspAl 291
               |   :::::::::         |||   |||      :::      |||      |||
Db        1402 CGTGAAGGTGAAGGTCCTAGAAGGCTTTCCTCGCCCCGTAGGTCCTGACTTCTTTGACTG 1461

Qy         291 aAla------------------------------PheIleCys----------------- 295
                |||                              |||   |||
Db        1462 TGCTGAGCCTGCCAATACTTTCCGCTGACAACACTTTGGATGCATTCAGGGGTACTGACT 1521

Qy         296 ----ProGlySerSerArgLeuHisIleMetAlaGlyArgArgLeuTrpTrpLeuAspLe 314
                   ||||||            |||:::         :::         ||||||   ||
Db        1522 CCTGCCAGGGCACTTAGAT---CATGTAAGAGACCCACAGCCATATCTGTGGCTCTGGCT 1578

Qy         314 uLysSerGlyAlaGlnAlaThrTrpThrGluLeuProTrpProHisGluLysValAspGl 334
               |::::::                              |||      :::
Db        1579 TCAGGCA------------------------------TGGGACAGACAG----------- 1597

Qy         334 yAlaLeuCysMetGluLysSerLeuGly-------------------------------- 343
                   ||||||:::   :::   :::|||
Db        1598 -GGCCTATGTCTCCTCAGGGGAGTGGGTTGGGGTGCAGCCACTGTTTGTAGGAACGACCA 1656

Qy         344 ----------------ProAsnSerCysSerAlaAsnGlyProGly 353
                                  |||:::|||         |||   |||
Db        1657 TGCTGTCATGTCACCTGCCAACAATTGTCTCAGACTAGGCAAAGGC 1702

RESULT 7
US-08-229-515A-12
; Sequence 12, Application US/08229515A
; Patent No. 5518885
;  GENERAL INFORMATION:
;    APPLICANT:  RAZIUDDIN
;    APPLICANT:  SARKAR, FAZLUL H
;    TITLE OF INVENTION:  ERBB2 PROMOTER BINDING PROTEIN IN
;    TITLE OF INVENTION:  NEOPLASTIC DISEASE
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NEEDLE & ROSENBERG PC
;      STREET:  127 Peachtree Street, Suite 1200
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  usa
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/229,515A
;      FILING DATE:  19 APR 1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PERRYMAN, DAVID G
;      REGISTRATION NUMBER:  33,438
;      REFERENCE/DOCKET NUMBER:  1414.608
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-688-0770
;      TELEFAX:  404-688-9880
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1717 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-229-515A-12

Alignment Scores:
Pred. No.:              7.71e-09       Length:        1717
Score:                  187.00         Matches:       52
Percent Similarity:     38.07%         Conservative:  23
Best Local Similarity:  26.40%         Mismatches:    48
Query Match:            8.56%          Indels:        74
DB:                     1              Gaps:          8

US-09-900-448-2 (1-391) x US-08-229-515A-12 (1-1717)

Qy          21 AlaIleAlaThrProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGluThr 40
               |||         |||:::|||      |||
Db         848 GCCACAGTGGTTCCTGTGCCCTCTGTCTCT------------------------------ 877

Qy          41 LysProAspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAlaThrThr 60
                  |||   |||:::         :::|||            ||||||||||||   |||
Db         878 ---CCAAAACCTGAGACCCCAGTCAAATGTGATCCTGCTTTGTCCTTTGATGCAGTCACC 934

Qy          61 LeuAspAspAsnGlyThrMetLeuPhePheLysGlyGluPheValTrpLysSerHisLys 80
               :::         |||      ||||||||||||            |||:::      :::
Db         935 ATG---CTGAGAGGGGAATTCCTATTCTTTAAAGACAGGCACTTCTGGCGTAGAACCCAG 991

Qy          81 TrpAspArgGlu------------LeuIleSerGluArgTrpLysAsnPheProSerPro 96
               |||:::   |||            |||||||||      |||   :::   ||||||
Db         992 TGGAATCCCGAGCCTGAATTCCATTTGATTTCAGCATTTTGGCCCTCTCTTCCTTCAGGC 1051

Qy          97 ValAspAlaAlaPheArgGlnGlyHis---AsnSerValPheLeuIleLysGlyAspLys 115
               :::|||||||||:::         :::   :::   |||   :::   ||||||   :::
Db        1052 TTAGATGCTGCCTATGAGGCAAATAACAAGGACAGAGTTCTGATTTTTAAAGGAAGTCAG 1111

Qy         116 ValTrpVal--------------------------------------------------- 118
                  |||
Db        1112 TTCTGGCAGTCCGAGGAAATGAAGTCCAAGCAGGTTACCCAAAGAGGATCCACACTCTT 1171

Qy         119 ---TyrProPro------------------------------------GluLysLys--- 124
                  :::||||||                                    |||||||||
Db        1172 GGCTTTCCTCCCACCGTGAAGAAGATTGATGCAGCTGTTTTTGAAAAGGAGAAGAAGAAG 1231

Qy         125 ---------------------------------------------------------Glu 125
                                                                        :::
Db        1232 ACGTATTTCTTTGTAGGTGACAAATACTGGAGATTTGATGAGACAAGACAGCTTATGGAT 1291

Qy         126 LysGlyTyrProLysLeuLeuGlnAspGluPheProGlyIleProSerProLeuAspAla 145
               ||||||:::|||:::|||:::   |||:::||||||||||||         :::||||||
Db        1292 AAAGGCTTCCCGAGACTGATAACAGATGACTTCCCAGGAATTGAGCCACAAGTTGATGCT 1351

Qy         146 AlaValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeuPhePhe 162
                  :::                        |||   |||      :::|||
Db        1352 GTGTTA---------------------CATGCATTTGGGTTTTTTTATTTC 1381

RESULT 8
US-08-645-865-12
; Sequence 12, Application US/08645865
; Patent No. 5654406
;  GENERAL INFORMATION:
;    APPLICANT:  RAZIUDDIN
;    APPLICANT:  SARKAR, FAZLUL H
;    TITLE OF INVENTION:  ERBB2 PROMOTER BINDING PROTEIN IN
;    TITLE OF INVENTION:  NEOPLASTIC DISEASE
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NEEDLE & ROSENBERG PC
;      STREET:  127 Peachtree Street, Suite 1200
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  usa
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/645,865
;      FILING DATE:  14 MAY 1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PERRYMAN, DAVID G
;      REGISTRATION NUMBER:  33,438
;      REFERENCE/DOCKET NUMBER:  1414.608
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-688-0770
;      TELEFAX:  404-688-9880
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1717 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-645-865-12

Alignment Scores:
Pred. No.:              7.71e-09       Length:        1717
Score:                  187.00         Matches:       52
Percent Similarity:     38.07%         Conservative:  23
Best Local Similarity:  26.40%         Mismatches:    48
Query Match:            8.56%          Indels:        74
DB:                     1              Gaps:          8

US-09-900-448-2 (1-391) x US-08-645-865-12 (1-1717)

Qy          21 AlaIleAlaThrProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGluThr 40
               |||         |||:::|||      |||
Db         848 GCCACAGTGGTTCCTGTGCCCTCTGTCTCT------------------------------ 877

Qy          41 LysProAspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAlaThrThr 60
                  |||   |||:::         :::|||            ||||||||||||   |||
Db         878 ---CCAAAACCTGAGACCCCAGTCAAATGTGATCCTGCTTTGTCCTTTGATGCAGTCACC 934

Qy          61 LeuAspAspAsnGlyThrMetLeuPhePheLysGlyGluPheValTrpLysSerHisLys 80
               :::         |||      ||||||||||||            |||:::      :::
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Db           935 ATG---CTGAGAGGGGAATTCCTATTCTTTAAAGACAGGCACTTCTGGCGTAGAACCCAG 991

Qy            81 TrpAspArgGlu------------LeuIleSerGluArgTrpLysAsnPheProSerPro 96
                 |||:::   |||            |||||||||      |||   :::   ||||||
Db           992 TGGAATCCCGAGCCTGAATTCCATTTGATTTCAGCATTTTGGCCCTCTCTTCCTTCAGGC 1051

Qy            97 ValAspAlaAlaPheArgGlnGlyHis---AsnSerValPheLeuIleLysGlyAspLys 115
                 :::|||||||||:::         :::   :::   |||   :::   ||||||   :::
Db          1052 TTAGATGCTGCCTATGAGGCAAATAACAAGGACAGAGTTCTGATTTTTAAAGGAAGTCAG 1111

Qy           116 ValTrpVal--------------------------------------------------- 118
                    |||
Db          1112 TTCTGGGCAGTCCGAGGAAATGAAGTCCAAGCAGGTTACCCAAAGAGGATCCACACTCTT 1171

Qy           119 ---TyrProPro------------------------------------GluLysLys--- 124
                    :::||||||                                    |||||||||
Db          1172 GGCTTTCCTCCCACCGTGAAGAAGATTGATGCAGCTGTTTTTGAAAAGGAGAAGAAGAAG 1231

Qy           125 ---------------------------------------------------------Glu 125
                                                                          :::
Db          1232 ACGTATTTCTTTGTAGGTGACAAATACTGGAGATTTGATGAGACAAGACAGCTTATGGAT 1291

Qy           126 LysGlyTyrProLysLeuLeuGlnAspGluPheProGlyIleProSerProLeuAspAla 145
                 ||||||:::|||:::|||:::   |||:::||||||||||||         :::||||||
Db          1292 AAAGGCTTCCCGAGACTGATAACAGATGACTTCCCAGGAATTGAGCCACAAGTTGATGCT 1351

Qy           146 AlaValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeuPhePhe 162
                    :::                        |||   |||      :::|||
Db          1352 GTGTTA----------------------CATGCATTTGGGTTTTTTATTTC 1381

RESULT 9
US-08-816-755-1
; Sequence 1, Application US/08816755
; Patent No. 5837508
;  GENERAL INFORMATION:
;    APPLICANT:  Arleth, Anthony
;    APPLICANT:  Arnold, Anne
;    APPLICANT:  Shabon, Usman
;    TITLE OF INVENTION:  No. 5837508el Membrane-Type Matrix
;    TITLE OF INVENTION:  Metalloproteinase-5 Gene
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corporation
;      STREET:  709 Swedeland Road
;      CITY:  King of Prussia
;      STATE:  PA
;      COUNTRY:
;      ZIP:  19406
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/816,755
;      FILING DATE:  05-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Han, William T
;      REGISTRATION NUMBER:  34,344
;      REFERENCE/DOCKET NUMBER:  GH50007
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-270-5219
;      TELEFAX:  610-270-4026
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3807 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-816-755-1

Alignment Scores:
Pred. No.:                3.88e-08        Length:          3807
Score:                    185.00          Matches:         87
Percent Similarity:       30.41%          Conservative:    31
Best Local Similarity:    22.42%          Mismatches:      123
Query Match:              8.47%           Indels:          147
DB:                       2               Gaps:            17

US-09-900-448-2 (1-391) x US-08-816-755-1 (1-3807)

Qy            25 ProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGluThrLysProAspPro 44
                 |||   ||||||:::                        |||:::            |||
Db           532 CCTCGGCCGCCCTCG-------------------------GGGACCGGCCATCCACACCA 567

Qy            45 AspValThrGluArgCysSerAspGlyTrpSerPheAspAlaThrThrLeuAspAspAsn 64
                                      ||||||                           :::
Db           568 GGCACCAAACCCAACATCTGTGACGGC---------------------------AACTTC 600

Qy            65 GlyThrMetLeuPhePheLysGlyGlu---PheValTrpLysSerHisLysTrpAspArg 83
                    |||:::      |||:::||||||   ||||||:::|||      :::|||
Db           601 AACACAGTGGCCCTCTTCCGGGGCGAGATGTTTGTCTTTAAGGAT---CGCTGGTTCTGG 657

Qy            84 GluLeu------------------------------------IleSerGluArgTrpLys 91
                    |||                                    |||   :::   ||||||
Db           658 CGTCTGCGCAATAACCGAGTGCAGGAGGGCTACCCCATGCAGATCGAGCAGTTCTGGAAG 717

Qy            92 AsnPheProSerProValAspAlaAlaPheArgGlnGlyHisAsnSerValPheLeuIle 111
                       |||:::   :::|||||||||:::   :::
Db           718 GGCCTGCCTGCCCGCATCGACGCAGCCTATGAAAGGGCCGATGGAGATTTGTCTTCTTC 777

Qy           112 LysGlyAspLysValTrpValTyrProProGluLysLysGluLysGlyTyrProLysLeu 131
                 ||||||||||||   ||||||:::               |||   |||||||||
Db           778 AAAGGTGACAAGTATTGGGTGTTTAAGGAGGTGACGGTGGAGCCTGGGTACCCCCACAGC 837

Qy           132 LeuGlnAspGluPheProGlyIleProSerProLeuAspAlaAlaValGluCysHisArg 151
                 |||   :::
Db           838 CTGGGGGAG------------------------------------------------CTG 849

Qy           152 GlyGluCysGlnAlaGluGlyValLeuPhePheGlnGlyHisGlyHisArgAsnGlyThr 171
                 |||   |||                                       |||   |||
Db           850 GGCAGCTGTTTGCCC---------------------------------CGTGAAGGC--- 873

Qy           172 GlyHisGlyAsnSerThrHisHisGlyProGluTyrMetArgCysSerProHisLeuVal 191
                                                                          :::
Db           874 ---------------------------------------------------------ATT 876

Qy           192 LeuSerAlaLeuThrSerAspAsnHisGlyAlaThrTyrAlaPheSerGlyThrHisTyr 211
                    :::||||||      :::      |||   ||||||   |||   |||      |||
Db           877 GACACAGCTCTGCGCTGGGAACCTGTGGGCAAGACCTACTTTTTCAAAGGCGAGCGGTAC 936

Qy           212 TrpArgLeuAspThrSerArg---------AspGlyTrpHisSerTrpProIleAlaHis 228
                 ||||||            |||         |||      :::      ||||||
Db           937 TGGCGCTACAGCGAGGAGCGGCGGCCACGGACCCTGGCTACCCTAAGCCCATCACC--- 993

Qy           229 GlnTrpProGlnGlyProSerAlaValAspAlaAlaPheSerTrpGluGlu------Lys 246
                    |||         |||   |||         ||||||      :::|||
Db           994 GTGTGGAAGGGCATCCCACAGGCTCCCCAAGGAGCCTTCATCAGCAAGGAAGGATATTAC 1053

Qy           247 LeuTyrLeuValGlnGlyThrGlnValTyrValPheLeuThrLysGlyGlyTyrThrLeu 266
                    |||      :::|||         :::   |||
Db          1054 ACCTATTTCTACAAGGGCCGGGACTACTGGAAGTTTGACAAC------------------ 1095

Qy           267 ValSerGlyTyrProLysArgLeuGluLysGluValGlyThrProHisGlyIleIleLeu 286
                                ::::::|||      |||   |||   |||      |||:::
Db          1096 ---------------CAGAAACTGAGCGTGGAGCCAGGCTACCCGCGCAACATCCTGCGT 1140

Qy           287 AspSerValAspAlaAlaPheIleCysProGlySerSerArgLeuHisIleMet-AlaGl 306
                 |||                                                ||| |||
Db          1141 GAC---------------------------------------------TGGATGGGCTGC 1155
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Qy         306 yArgArgLeuTrpTrpLeuAspLeuLysSerGlyAla------GlnAlaThrTrpThrGl 324
                   |||      |||         :::||||||         :::   |||||||||
Db        1156 AACCAGAAGGAGGTGGAGCGGCGGAAGGAGCGGCGGCTGCCCAGGACGACGTGGACATC 1215

Qy         324 u---------------------------------LeuProTrpProHisGluLysValAs 333
                                                    |||||||||
Db        1216 ATGGTGACCATCAACGATGTGCCGGGCTCCGTGAACGCCGTGGCCGTGGTCA-------- 1267

Qy         333 pGlyAlaLeuCysMetGluLysSerLeuGlyProAsnSerCysSerAlaAsnGlyProGl 353
                                              |||   ||||||   :::
Db        1268 ----------------------------TCCCCTGCATCCTGTCCCTCTGCATCC----- 1294

Qy         353 yLeuTyrLeuIleHisGlyProAsnLeuTyrCysTyrSerAspValGluLysLeuAsnAl 373
                                           :::|||:::|||               :::
Db        1295 ----------------------------TGGTGCTGGTCTACACCATCTTCCAGTTCAAG 1326

Qy         373 aAlaLysAlaLeuProGlnPro 380
                   :::      |||||||||
Db        1327 AACAAGACAAGGCCCTCAGCCT 1348

RESULT 10
US-09-090-673-1
; Sequence 1, Application US/09090673
; Patent No. 6214600
;  GENERAL INFORMATION:
;    APPLICANT:  Arleth, Anthony
;    APPLICANT:  Arnold, Anne
;    APPLICANT:  Shabon, Usman
;    TITLE OF INVENTION:  No. 6214600el Membrane-Type Matrix
;    TITLE OF INVENTION:  Metalloproteinase-5 Gene
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ratner & Prestia
;      STREET:  P.O. Box 980
;      CITY:  Valley Forge
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/090,673
;      FILING DATE:  3-June-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Prestia, Paul F.
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  GH50007-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0701
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3807 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-090-673-1

Alignment Scores:
Pred. No.:              3.88e-08      Length:          3807
Score:                  185.00        Matches:         87
Percent Similarity:     30.41%        Conservative:    31
Best Local Similarity:  22.42%        Mismatches:      123

Query Match:            8.47%         Indels:          147
DB:                     3             Gaps:            17

US-09-900-448-2 (1-391) x US-09-090-673-1 (1-3807)

Qy          25 ProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGluThrLysProAspPro 44
               |||   ||||||:::                        |||:::            |||
Db         532 CCTCGGCCGCCCTCG------------------------GGGGACCGGCCATCCACACCA 567

Qy          45 AspValThrGluArgCysSerAspGlyTrpSerPheAspAlaThrThrLeuAspAspAsn 64
                                    ||||||                           :::
Db         568 GGCACCAAACCCAACATCTGTGACGGC---------------------------AACTTC 600

Qy          65 GlyThrMetLeuPhePheLysGlyGlu---PheValTrpLysSerHisLysTrpAspArg 83
                  |||:::      |||:::||||||   ||||||:::|||      :::|||
Db         601 AACACAGTGGCCCTCTTCCGGGGCGAGATGTTTGTCTTTAAGGAT---CGCTGGTTCTGG 657

Qy          84 GluLeu------------------------------------IleSerGluArgTrpLys 91
                  |||                                    |||   :::   ||||||
Db         658 CGTCTGCGCAATAACCGAGTGCAGGAGGGCTACCCCATGCAGATCGAGCAGTTCTGGAAG 717

Qy          92 AsnPheProSerProValAspAlaAlaPheArgGlnGlyHisAsnSerValPheLeuIle 111
                     |||:::   :::|||||||||:::   :::
Db         718 GGCCTGCCTGCCCGCATCGACGCAGCCTATGAAAGGGCCGATGGGAGATTTGTCTTCTTC 777

Qy         112 LysGlyAspLysValTrpValTyrProProGluLysLysGluLysGlyTyrProLysLeu 131
               ||||||||||||   ||||||:::               |||   |||||||||
Db         778 AAAGGTGACAAGTATTGGGTGTTTAAGGAGGTGACGGTGGAGCCTGGGTACCCCCACAGC 837

Qy         132 LeuGlnAspGluPheProGlyIleProSerProLeuAspAlaAlaValGluCysHisArg 151
               |||   :::
Db         838 CTGGGGAG-------------------------------------------------CTG 849

Qy         152 GlyGluCysGlnAlaGluGlyValLeuPhePheGlnGlyHisGlyHisArgAsnGlyThr 171
               |||   |||                                       |||   |||
Db         850 GGCAGCTGTTTGCCC---------------------------------CGTGAAGGC--- 873

Qy         172 GlyHisGlyAsnSerThrHisHisGlyProGluTyrMetArgCysSerProHisLeuVal 191
                                                                        :::
Db         874 ---------------------------------------------------------ATT 876

Qy         192 LeuSerAlaLeuThrSerAspAsnHisGlyAlaThrTyrAlaPheSerGlyThrHisTyr 211
                  :::||||||      :::      |||   ||||||   |||   |||      |||
Db         877 GACACAGCTCTGCGCTGGGAACCTGTGGGCAAGACCTACTTTTTCAAAGGCGAGCGGTAC 936

Qy         212 TrpArgLeuAspThrSerArg---------AspGlyTrpHisSerTrpProIleAlaHis 228
               ||||||            |||         |||      :::      ||||||
Db         937 TGGCGCTACAGCGAGGAGCGGCGGGCCACGGACCCTGGCTACCCTAAGCCCATCACC--- 993

Qy         229 GlnTrpProGlnGlyProSerAlaValAspAlaAlaPheSerTrpGluGlu------Lys 246
                  |||         |||   |||         ||||||      :::|||
Db         994 GTGTGGAAGGGCATCCCACAGGCTCCCCAAGGAGCCTTCATCAGCAAGGAAGGATATTAC 1053

Qy         247 LeuTyrLeuValGlnGlyThrGlnValTyrValPheLeuThrLysGlyGlyTyrThrLeu 266
                  |||      :::|||         :::   |||
Db        1054 ACCTATTTCTACAAGGGCCGGGACTACTGGAAGTTTGACAAC------------------ 1095

Qy         267 ValSerGlyTyrProLysArgLeuGluLysGluValGlyThrProHisGlyIleIleLeu 286
                              ::::::|||      |||   |||   |||      |||:::
Db        1096 ---------------CAGAAACTGAGCGTGGAGCCAGGCTACCCGCGCAACATCCTGCGT 1140

Qy         287 AspSerValAspAlaAlaPheIleCysProGlySerSerArgLeuHisIleMet-AlaGl 306
               |||                                                ||| |||
Db        1141 GAC---------------------------------------------TGGATGGGCTGC 1155

Qy         306 yArgArgLeuTrpTrpLeuAspLeuLysSerGlyAla------GlnAlaThrTrpThrGl 324
                   |||      |||         :::||||||         :::   |||||||||
Db        1156 AACCAGAAGGAGGTGGAGCGGCGGAAGGAGCGGCGGCTGCCCAGGACGACGTGGACATC 1215

Qy         324 u---------------------------------LeuProTrpProHisGluLysValAs 333
                                                    |||||||||
Db        1216 ATGGTGACCATCAACGATGTGCCGGGCTCCGTGAACGCCGTGGCCGTGGTCA-------- 1267
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Qy         333 pGlyAlaLeuCysMetGluLysSerLeuGlyProAsnSerCysSerAlaAsnGlyProGl 353
                                              |||   ||||||   :::
Db        1268 ----------------------------TCCCCTGCATCCTGTCCCTCTGCATCC----- 1294

Qy         353 yLeuTyrLeuIleHisGlyProAsnLeuTyrCysTyrSerAspValGluLysLeuAsnAl 373
                                           :::|||:::|||               :::
Db        1295 ----------------------------TGGTGCTGGTCTACACCATCTTCCAGTTCAAG 1326

Qy         373 aAlaLysAlaLeuProGlnPro 380
                   :::      |||||||||
Db        1327 AACAAGACAAGGCCCTCAGCCT 1348

RESULT 11
US-09-178-002-3
; Sequence 3, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
;  APPLICANT: Hu, Shou-Ih
;  TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
;  FILE REFERENCE: CGC 2048
;  CURRENT APPLICATION NUMBER: US/09/178,002
;  CURRENT FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 2223
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (72)..(1475)
US-09-178-002-3

Alignment Scores:
Pred. No.:             2.49e-08        Length:        2223
Score:                 183.50          Matches:       60
Percent Similarity:    36.99%          Conservative:  31
Best Local Similarity: 24.39%          Mismatches:    80
Query Match:           8.40%           Indels:        75
DB:                    1               Gaps:          10

US-09-900-448-2 (1-391) x US-09-178-002-3 (1-2223)

Qy          23 AlaThrProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGluThrLysPro 42
               :::   |||:::   ||||||                        |||   :::   |||
Db         864 AGCAACCCTATCCAACCTACT------------------------GGACCAAGCACACCC 899

Qy          43 AspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAla---ThrThrLeu 61
                  |||               |||            :::|||||||||   |||||||||
Db         900 AAACCC---------------TGTGACCCCAGTTTGACATTTGATGCTATCACCACACTC 944

Qy          62 AspAspAsnGlyThrMetLeuPhePheLysGlyGluPheValTrpLysSerHis------ 79
                        |||   :::||||||||||||      :::   |||:::   |||
Db         945 ------CGTGGAGAAATACTTTTCTTTAAAGACAGGTACTTCTGGAGAAGGCATCCTCAG 998

Qy          80 ------LysTrpAspArgGluLeuIleSerGluArgTrpLysAsnPheProSerProVal 97
                     :::   :::         ||||||      |||   :::   |||:::   :::
Db         999 CTACAAAGAGTCGAAATGAATTTTATTTCTCTATTCTGGCCATCCCTTCCAACTGGTATA 1058

Qy          98 AspAlaAlaPheArgGln---GlyHisAsnSerValPheLeuIleLysGlyAspLysVal 116
                  ||||||:::               :::   :::||||||   ||||||::::::
Db        1059 CAGGCTGCTTATGAAGATTTTGACAGAGACCTCATTTTCCTATTTAAAGGCAACCAATAC 1118

Qy         117 TrpValTyrProProGluLysLysGluLysGlyTyrProLysLeuLeuGlnAsp---Glu 135
               |||                        :::||||||||||||   :::   :::
Db        1119 TGGGCTCTGAGTGGCTATGATATTCTGCAAGGTTATCCCAAGGATATATCAAACTATGGC 1178

Qy         136 PheProGlyIleProSerProLeuAspAlaAlaValGluCysHisArgGlyGluCysGln 155
               ||||||               :::||||||||||||
Db        1179 TTCCCCAGCAGCGTCCAAGCAATTGACGCAGCTGTT------------------------ 1214

Qy         156 AlaGluGlyValLeuPhePheGlnGlyHisGlyHisArgAsnGlyThrGlyHisGlyAsn 175
                              |||::::::
Db        1215 ---------------TTCTACAGA------------------------------------ 1223

Qy         176 SerThrHisHisGlyProGluTyrMetArgCysSerProHisLeuValLeuSerAlaLeu 195

Db        1223 ------------------------------------------------------------ 1223

Qy         196 ThrSerAspAsnHisGlyAlaThrTyrAlaPheSerGlyThrHisTyrTrpArgLeuAsp 215
                                    ||||||   |||            :::||||||   |||
Db        1224 ---------------AGTAAAACATACTTCTTTGTAAATGACCAATTCTGGAGATATGAT 1268

Qy         216 ThrSerArg---------AspGlyTrpHisSerTrpProIleAlaHisGlnTrpProGln 232
                     |||         :::      :::         |||:::      :::|||
Db        1269 AACCAAAGACAATTCATGGAGCCAGGTTATCCCAAAAGCATATCAGGTGCCTTTCCAGGA 1328

Qy         233 GlyProSerAlaValAspAlaAlaPheSerTrpGluGluLysLeuTyrLeuValGlnGly 252
                     |||   |||||||||   |||      |||         ::::::      |||
Db        1329 ATAGAGAGTAAAGTTGATGCAGTTTTCCAGCAAGAACATTTCTTCCATGTCTTCAGTGGA 1388

Qy         253 ThrGlnValTyrValPhe 258
                  :::   |||   |||
Db        1389 CCAAGATATTACGCATTT 1406

RESULT 12
US-09-023-655-1040
; Sequence 1040, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,655
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1040:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2223 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g180617
US-09-023-655-1040

Alignment Scores:
Pred. No.:              2.49e-08       Length:         2223
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Score:                   183.50         Matches:        60
Percent Similarity:      36.99%         Conservative:   31
Best Local Similarity:   24.39%         Mismatches:     80
Query Match:             8.40%          Indels:         75
DB:                      4              Gaps:           10

US-09-900-448-2 (1-391) x US-09-023-655-1040 (1-2223)

Qy           23 AlaThrProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGluThrLysPro 42
                :::   |||:::   ||||||                        |||   :::   |||
Db          864 AGCAACCCTATCCAACCTACT------------------------GGACCAAGCACACCC 899

Qy           43 AspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAla---ThrThrLeu 61
                   |||               |||            :::|||||||||   |||||||||
Db          900 AAACCC---------------TGTGACCCCAGTTTGACATTTGATGCTATCACCACACTC 944

Qy           62 AspAspAsnGlyThrMetLeuPhePheLysGlyGluPheValTrpLysSerHis------ 79
                         |||   :::||||||||||||      :::   |||:::   |||
Db          945 ------CGTGGAGAAATACTTTTCTTTAAAGACAGGTACTTCTGGAGAAGGCATCCTCAG 998

Qy           80 ------LysTrpAspArgGluLeuIleSerGluArgTrpLysAsnPheProSerProVal 97
                      :::   :::         ||||||      |||   :::   |||:::   :::
Db          999 CTACAAAGAGTCGAAATGAATTTTATTTCTCTATTCTGGCCATCCCTTCCAACTGGTATA 1058

Qy           98 AspAlaAlaPheArgGln---GlyHisAsnSerValPheLeuIleLysGlyAspLysVal 116
                   ||||||:::               :::   :::||||||   ||||||::::::
Db         1059 CAGGCTGCTTATGAAGATTTTGACAGAGACCTCATTTTCCTATTTAAAGGCAACCAATAC 1118

Qy          117 TrpValTyrProProGluLysLysGluLysGlyTyrProLysLeuLeuGlnAsp---Glu 135
                |||                        :::||||||||||||   :::   :::
Db         1119 TGGGCTCTGAGTGGCTATGATATTCTGCAAGGTTATCCCAAGGATATATCAAACTATGGC 1178

Qy          136 PheProGlyIleProSerProLeuAspAlaAlaValGluCysHisArgGlyGluCysGln 155
                ||||||               :::||||||||||||
Db         1179 TTCCCCAGCAGCGTCCAAGCAATTGACGCAGCTGTT------------------------ 1214

Qy          156 AlaGluGlyValLeuPhePheGlnGlyHisGlyHisArgAsnGlyThrGlyHisGlyAsn 175
                               |||::::::
Db         1215 ---------------TTCTACAGA------------------------------------ 1223

Qy          176 SerThrHisHisGlyProGluTyrMetArgCysSerProHisLeuValLeuSerAlaLeu 195

Db         1223 ------------------------------------------------------------ 1223

Qy          196 ThrSerAspAsnHisGlyAlaThrTyrAlaPheSerGlyThrHisTyrTrpArgLeuAsp 215
                                     ||||||   |||            :::||||||   |||
Db         1224 ---------------AGTAAAACATACTTCTTTGTAAATGACCAATTCTGGAGATATGAT 1268

Qy          216 ThrSerArg---------AspGlyTrpHisSerTrpProIleAlaHisGlnTrpProGln 232
                      |||         :::      :::         |||:::      :::|||
Db         1269 AACCAAAGACAATTCATGGAGCCAGGTTATCCCAAAAGCATATCAGGTGCCTTTCCAGGA 1328

Qy          233 GlyProSerAlaValAspAlaAlaPheSerTrpGluGluLysLeuTyrLeuValGlnGly 252
                      |||   |||||||||   |||      |||         ::::::      |||
Db         1329 ATAGAGAGTAAAGTTGATGCAGTTTTCCAGCAAGAACATTTCTTCCATGTCTTCAGTGGA 1388

Qy          253 ThrGlnValTyrValPhe 258
                   :::   |||   |||
Db         1389 CCAAGATATTACGCATTT 1406

RESULT 13
US-09-023-655-1410
; Sequence 1410, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
```

```
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,655
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1410:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2247 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g456256
US-09-023-655-1410

Alignment Scores:
Pred. No.:               2.53e-08       Length:         2247
Score:                   183.50         Matches:        85
Percent Similarity:      30.15%         Conservative:   32
Best Local Similarity:   21.91%         Mismatches:     130
Query Match:             8.40%          Indels:         141
DB:                      4              Gaps:           20

US-09-900-448-2 (1-391) x US-09-023-655-1410 (1-2247)

Qy           13 LeuTrpSerLeuCysTrpSerLeuAlaIleAlaThrProLeuProProThrSerAlaHis 32
                |||:::         |||         :::   :::      |||
Db          775 CTATATGGCCAGCCCTGGCCC---ACTGTCACCTCCAGGACCCCAGCCCTGGGCCCCCAG 831

Qy           33 GlyAsnValAlaGluGlyGluThrLysPro---AspProAspValThrGluArgCysSer 51
                      :::         |||      |||   :::||||||
Db          832 GCTGGGATAGACACCAATGAGATTGCACCGCTGGAGCCAGACGCCCCGCCAGATGCCTGT 891

Qy           52 AspGlyTrpSerPheAspAlaThrThrLeuAspAspAsnGlyThrMetLeuPhePheLys 71
                :::      ||||||||||||   :::            |||   :::   |||||||||
Db          892 GAGGCC---TCCTTTGACGCGGTCTCC---ACCATCCGAGGCGAGCTCTTTTTCTTCAAA 945

Qy           72 GlyGluPheValTrpLysSerHisLysTrpAspArgGlu---------------LeuIle 86
                      |||||||||:::                  :::               |||
Db          946 GCGGGCTTTGTGTGGCGCCTCCGTGGGGGCCAGCTGCAGCCCGGCTACCCAGCATTGGCC 1005

Qy           87 SerGluArgTrpLysAsnPheProSerProValAspAlaAlaPheArgGlnGlyHisAsn 106
                |||      |||:::      ||||||||||||||||||||||||
Db         1006 TCTCGCCACTGGCAGGGACTGCCCAGCCCTGTGGACGCTGCCTTCGAGGATGCCCAGGGC 1065

Qy          107 SerValPheLeuIleLysGlyAspLysValTrpValTyrProProGluLysLysGluLys 126
                   ::::::      :::|||   :::   |||||||||      ||||||
Db         1066 CACATTTGGTTCTTCCAAGGTGCTCAGTACTGGGTGTACGACGGTGAAAAGCCAGTCCTG 1125

Qy          127 GlyTyrProLysLeuLeuGlnAspGluPheProGlyIleProSerProLeuAspAlaAla 146
                |||                                    |||:::||||||
Db         1126 GGC------------------------------------CCCGCACCCCTCACCGAGCTG 1149
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Qy         147 ValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeuPhePheGlnGlyHisGly 166
                                                |||::::::   |||      |||
Db        1150 ---------------------------------GGCCTGGTGAGGTTCCCGGTCCATGCT 1176

Qy         167 HisArgAsnGlyThrGlyHisGlyAsnSerThrHisHisGlyProGluTyrMetArgCys 186
                                          :::         |||||||||
Db        1177 ---------------------------GCCTTGGTCTGGGGTCCCGAG------------ 1197

Qy         187 SerProHisLeuValLeuSerAlaLeuThrSerAspAsnHisGlyAlaThrTyrAlaPhe 206
                                                                  |||   |||
Db        1198 ---------------------------------------AAGAACAAGATCTACTTCTTC 1218

Qy         207 SerGlyThrHisTyrTrpArgLeuAspThrSerArgAspGlyTrpHisSerTrpProIle 226
                  |||      |||||||||         |||               |||   |||:::
Db        1219 CGAGGCAGGGACTACTGGCGTTTCCACCCCAGCACCCGGCGTGTAGACAGT---CCCGTG 1275

Qy         227 ---------AlaHisGlnTrpProGlnGlyProSerAlaValAspAlaAlaPheSerTrp 243
                        |||      |||         ||||||   :::||||||||||||
Db        1276 CCCCGCAGGGCCACTGACTGGAGAGGGGTGCCCTCTGAGATCGACGCTGCCTTC------ 1329

Qy         244 GluGluLysLeuTyrLeuValGlnGlyThrGlnValTyrValPheLeuThrLysGly--- 262
                                    |||            |||   :::      :::|||
Db        1330 ---------------------CAGGATGCTGATGGCTATGCCTACTTCCTGCGCGGCCGC 1368

Qy         263 ------------------------GlyTyrThrLeuValSerGlyTyrProLysArgLeu 274
                                                   :::   |||:::|||:::   :::
Db        1369 CTCTACTGGAAGTTTGACCCTGTGAAGGTGAAGGCTCTGGAAGGCTTCCCCCGTCTCGTG 1428

Qy         275 GluLysGlu---------------------------------------------ValGly 279
                     :::                                             :::|||
Db        1429 GGTCCTGACTTCTTTGGCTGTGCCGAGCCTGCCAACACTTTCCTCTGACCATGGCTTGGA 1488

Qy         280 ThrProHisGlyIleIleLeuAspSerValAspAlaAlaPheIleCys---------Pro 296
                  |||   |||                                 |||         |||
Db        1489 TGCCCTCAGGGG---------------------------------TGCTGACCCCTGCCA 1515

Qy         297 GlySerSerArgLeuHisIleMetAlaGlyArgArgLeuTrp---------TrpLeuAsp 313
               |||            |||            |||      |||         ||||||
Db        1516 GGC------------CACGAATATCAGGCTAGAGACCCATGGCCATCTTTGTGGCTG--- 1560

Qy         314 LeuLysSerGlyAlaGlnAlaThrTrpThrGluLeuProTrpProHisGluLysValAsp 333
                                       |||
Db        1561 ------------------------TGGGCA------------------------------ 1566

Qy         334 GlyAlaLeuCysMetGluLysSerLeuGlyProAsnSerCysSerAlaAsnGlyProGly 353
                                       :::|||   :::   |||         |||   |||
Db        1567 ------------------CCAGGCATGGGACTGAGCCCATGTCTCCTGCAGGGGGATGGG 1608

Qy         354 LeuTyrLeuIleHisGlyProAsn 361
               :::         |||      |||
Db        1609 GTGGGGTACAACCACCATGACAAC 1632

RESULT 14
US-07-794-393-1
; Sequence 1, Application US/07794393
; Patent No. 5236844
;  GENERAL INFORMATION:
;    APPLICANT:  CHAMBON, PIERRE
;    APPLICANT:  BASSET, PAUL
;    APPLICANT:  BELLOCQ, JEAN-PIERRE
;    TITLE OF INVENTION:  ANALYTICAL MARKERS FOR MALIGNANT BREAST
;    TITLE OF INVENTION:  CANCER
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1225 Connecticut Ave. NW Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/794,393
;      FILING DATE:  19911121
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9025326.1
;      FILING DATE:  21-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GOLDSTEIN, JORGE A
;      REGISTRATION NUMBER:  29,021
;      REFERENCE/DOCKET NUMBER:  1383.0040000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 466-0800
;      TELEFAX:  (202) 833-8716
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2256 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  10..1473
US-07-794-393-1

Alignment Scores:
Pred. No.:              2.54e-08        Length:         2256
Score:                  183.50          Matches:        85
Percent Similarity:     30.15%          Conservative:   32
Best Local Similarity:  21.91%          Mismatches:     130
Query Match:            8.40%           Indels:         141
DB:                     1               Gaps:           20

US-09-900-448-2 (1-391) x US-07-794-393-1 (1-2256)

Qy          13 LeuTrpSerLeuCysTrpSerLeuAlaIleAlaThrProLeuProProThrSerAlaHis 32
               |||:::         |||         :::   :::      |||
Db         775 CTATATGGCCAGCCCTGGCCC---ACTGTCACCTCCAGGACCCCAGCCCTGGGCCCCCAG 831

Qy          33 GlyAsnValAlaGluGlyGluThrLysPro---AspProAspValThrGluArgCysSer 51
                     :::         |||      |||   :::||||||
Db         832 GCTGGGATAGACACCAATGAGATTGCACCGCTGGAGCCAGACGCCCCGCCAGATGCCTGT 891

Qy          52 AspGlyTrpSerPheAspAlaThrThrLeuAspAspAsnGlyThrMetLeuPhePheLys 71
               :::      ||||||||||||   :::            |||   :::   |||||||||
Db         892 GAGGCC---TCCTTTGACGCGGTCTCC---ACCATCCGAGGCGAGCTCTTTTTCTTCAAA 945

Qy          72 GlyGluPheValTrpLysSerHisLysTrpAspArgGlu---------------LeuIle 86
                     |||||||||:::                  :::               |||
Db         946 GCGGGCTTTGTGTGGCGCCTCCGTGGGGGCCAGCTGCAGCCCGGCTACCCAGCATTGGCC 1005

Qy          87 SerGluArgTrpLysAsnPheProSerProValAspAlaAlaPheArgGlnGlyHisAsn 106
               |||      |||:::      ||||||||||||||||||||||||
Db        1006 TCTCGCCACTGGCAGGGACTGCCCAGCCCTGTGGACGCTGCCTTCGAGGATGCCCAGGGC 1065

Qy         107 SerValPheLeuIleLysGlyAspLysValTrpValTyrProProGluLysLysGluLys 126
                  ::::::      :::|||   :::   |||||||||      ||||||
Db        1066 CACATTTGGTTCTTCCAAGGTGCTCAGTACTGGGTGTACGACGGTGAAAAGCCAGTCCTG 1125

Qy         127 GlyTyrProLysLeuLeuGlnAspGluPheProGlyIleProSerProLeuAspAlaAla 146
               |||                                    |||:::||||||
Db        1126 GGC------------------------------------CCCGCACCCCTCACCGAGCTG 1149

Qy         147 ValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeuPhePheGlnGlyHisGly 166
                                                |||::::::   |||      |||
Db        1150 ---------------------------------GGCCTGGTGAGGTTCCCGGTCCATGCT 1176

Qy         167 HisArgAsnGlyThrGlyHisGlyAsnSerThrHisHisGlyProGluTyrMetArgCys 186
                                          :::         |||||||||
Db         1177 ---------------------------GCCTTGGTCTGGGGTCCCGAG------------ 1197

Qy          187 SerProHisLeuValLeuSerAlaLeuThrSerAspAsnHisGlyAlaThrTyrAlaPhe 206
                                                                   |||   |||
Db         1198 ---------------------------------------AAGAACAAGATCTACTTCTTC 1218

Qy          207 SerGlyThrHisTyrTrpArgLeuAspThrSerArgAspGlyTrpHisSerTrpProIle 226
                   |||      |||||||||         |||               |||   |||:::
Db         1219 CGAGGCAGGGACTACTGGCGTTTCCACCCCAGCACCCGGCGTGTAGACAGT---CCCGTG 1275

Qy          227 ---------AlaHisGlnTrpProGlnGlyProSerAlaValAspAlaAlaPheSerTrp 243
                         |||      |||         ||||||   :::||||||||||||
Db         1276 CCCCGCAGGGCCACTGACTGGAGAGGGGTGCCCTCTGAGATCGACGCTGCCTTC------ 1329

Qy          244 GluGluLysLeuTyrLeuValGlnGlyThrGlnValTyrValPheLeuThrLysGly--- 262
                                     |||            |||   :::      :::|||
Db         1330 ---------------------CAGGATGCTGATGGCTATGCCTACTTCCTGCGCGGCCGC 1368

Qy          263 ------------------------GlyTyrThrLeuValSerGlyTyrProLysArgLeu 274
                                                    :::   |||:::|||:::   :::
Db         1369 CTCTACTGGAAGTTTGACCCTGTGAAGGTGAAGGCTCTGGAAGGCTTCCCCCGTCTCGTG 1428

Qy          275 GluLysGlu---------------------------------------------ValGly 279
                      :::                                             :::|||
Db         1429 GGTCCTGACTTCTTTGGCTGTGCCGAGCCTGCCAACACTTTCCTCTGACCATGGCTTGGA 1488

Qy          280 ThrProHisGlyIleIleLeuAspSerValAspAlaAlaPheIleCys---------Pro 296
                   |||   |||                                 |||         |||
Db         1489 TGCCCTCAGGGG---------------------------------TGCTGACCCCTGCCA 1515

Qy          297 GlySerSerArgLeuHisIleMetAlaGlyArgArgLeuTrp---------TrpLeuAsp 313
                |||            |||            |||      |||         ||||||
Db         1516 GGC------------CACGAATATCAGGCTAGAGACCCATGGCCATCTTTGTGGCTG--- 1560

Qy          314 LeuLysSerGlyAlaGlnAlaThrTrpThrGluLeuProTrpProHisGluLysValAsp 333
                                        |||
Db         1561 ------------------------TGGGCA------------------------------ 1566

Qy          334 GlyAlaLeuCysMetGluLysSerLeuGlyProAsnSerCysSerAlaAsnGlyProGly 353
                                        :::|||   :::   |||         |||   |||
Db         1567 ------------------CCAGGCATGGGACTGAGCCCATGTCTCCTGCAGGGGGATGGG 1608

Qy          354 LeuTyrLeuIleHisGlyProAsn 361
                :::         |||      |||
Db         1609 GTGGGGTACAACCACCATGACAAC 1632

RESULT 15
US-08-001-711-1
; Sequence 1, Application US/08001711
; Patent No. 5484726
;  GENERAL INFORMATION:
;    APPLICANT:  BASSET, PAUL
;    APPLICANT:  BELLOCQ, JEAN-PIERRE
;    APPLICANT:  CHAMBON, PIERRE
;    TITLE OF INVENTION:  ANALYTICAL MARKERS FOR MALIGNANT BREAST
;    TITLE OF INVENTION:  CANCER
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1225 Connecticut Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/001,711
;      FILING DATE:  19930107
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/794,393
;      FILING DATE:  11-NOV-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9025626.1
;      FILING DATE:  21-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MILLMAN, ROBERT A
;      REGISTRATION NUMBER:  36,217
;      REFERENCE/DOCKET NUMBER:  1383.0040001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)466-0800
;      TELEFAX:  (202)833-8716
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2256 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  10..1473
US-08-001-711-1

Alignment Scores:
Pred. No.:              2.54e-08       Length:         2256
Score:                  183.50         Matches:        85
Percent Similarity:     30.15%         Conservative:   32
Best Local Similarity:  21.91%         Mismatches:     130
Query Match:            8.40%          Indels:         141
DB:                     1              Gaps:           20

US-09-900-448-2 (1-391) x US-08-001-711-1 (1-2256)

Qy           13 LeuTrpSerLeuCysTrpSerLeuAlaIleAlaThrProLeuProProThrSerAlaHis 32
                |||:::         |||         :::   :::      |||
Db          775 CTATATGGCCAGCCCTGGCCC---ACTGTCACCTCCAGGACCCCAGCCCTGGGCCCCCAG 831

Qy           33 GlyAsnValAlaGluGlyGluThrLysPro---AspProAspValThrGluArgCysSer 51
                      :::         |||      |||   :::||||||
Db          832 GCTGGGATAGACACCAATGAGATTGCACCGCTGGAGCCAGACGCCCCGCCAGATGCCTGT 891

Qy           52 AspGlyTrpSerPheAspAlaThrThrLeuAspAspAsnGlyThrMetLeuPhePheLys 71
                :::      ||||||||||||   :::            |||   :::   |||||||||
Db          892 GAGGCC---TCCTTTGACGCGGTCTCC---ACCATCCGAGGCGAGCTCTTTTTCTTCAAA 945

Qy           72 GlyGluPheValTrpLysSerHisLysTrpAspArgGlu---------------LeuIle 86
                      |||||||||:::                  :::               |||
Db          946 GCGGGCTTTGTGTGGCGCCTCCGTGGGGGCCAGCTGCAGCCCGGCTACCCAGCATTGGCC 1005

Qy           87 SerGluArgTrpLysAsnPheProSerProValAspAlaAlaPheArgGlnGlyHisAsn 106
                |||      |||:::      ||||||||||||||||||||||||
Db         1006 TCTCGCCACTGGCAGGGACTGCCCAGCCCTGTGGACGCTGCCTTCGAGGATGCCCAGGGC 1065

Qy          107 SerValPheLeuIleLysGlyAspLysValTrpValTyrProProGluLysLysGluLys 126
                   ::::::      :::|||   :::   |||||||||      ||||||
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Qy          127 GlyTyrProLysLeuLeuGlnAspGluPheProGlyIleProSerProLeuAspAlaAla 146
                |||                                    |||:::||||||
Db         1126 GGC------------------------------------CCCGCACCCCTCACCGAGCTG 1149

Qy          147 ValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeuPhePheGlnGlyHisGly 166
                                                 |||::::::   |||      |||
Db         1150 ---------------------------------GGCCTGGTGAGGTTCCCGGTCCATGCT 1176

Qy          167 HisArgAsnGlyThrGlyHisGlyAsnSerThrHisHisGlyProGluTyrMetArgCys 186
                                           :::         |||||||||
Db         1177 ---------------------------GCCTTGGTCTGGGGTCCCGAG------------ 1197

Qy          187 SerProHisLeuValLeuSerAlaLeuThrSerAspAsnHisGlyAlaThrTyrAlaPhe 206
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Db         1198 ---------------------------------------AAGAACAAGATCTACTTCTTC 1218
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Qy         207 SerGlyThrHisTyrTrpArgLeuAspThrSerArgAspGlyTrpHisSerTrpProIle 226
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Db        1219 CGAGGCAGGGACTACTGGCGTTTCCACCCCAGCACCCGGCGTGTAGACAGT---CCCGTG 1275

Qy         227 ---------AlaHisGlnTrpProGlnGlyProSerAlaValAspAlaAlaPheSerTrp 243
                        |||      |||         ||||||   :::||||||||||||
Db        1276 CCCCGCAGGGCCACTGACTGGAGAGGGGTGCCCTCTGAGATCGACGCTGCCTTC------ 1329

Qy         244 GluGluLysLeuTyrLeuValGlnGlyThrGlnValTyrValPheLeuThrLysGly--- 262
                                    |||            |||   :::      :::|||
Db        1330 ---------------------CAGGATGCTGATGGCTATGCCTACTTCCTGCGCGGCCGC 1368

Qy         263 ------------------------GlyTyrThrLeuValSerGlyTyrProLysArgLeu 274
                                                   :::   |||:::|||:::   :::
Db        1369 CTCTACTGGAAGTTTGACCCTGTGAAGGTGAAGGCTCTGGAAGGCTTCCCCCGTCTCGTG 1428

Qy         275 GluLysGlu---------------------------------------------ValGly 279
                     :::                                             :::|||
Db        1429 GGTCCTGACTTCTTTGGCTGTGCCGAGCCTGCCAACACTTTCCTCTGACCATGGCTTGGA 1488

Qy         280 ThrProHisGlyIleIleLeuAspSerValAspAlaAlaPheIleCys---------Pro 296
                  |||   |||                                 |||         |||
Db        1489 TGCCCTCAGGGG---------------------------------TGCTGACCCCTGCCA 1515

Qy         297 GlySerSerArgLeuHisIleMetAlaGlyArgArgLeuTrp---------TrpLeuAsp 313
               |||            |||            |||      |||         ||||||
Db        1516 GGC------------CACGAATATCAGGCTAGAGACCCATGGCCATCTTTGTGGCTG--- 1560

Qy         314 LeuLysSerGlyAlaGlnAlaThrTrpThrGluLeuProTrpProHisGluLysValAsp 333
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Db        1561 ------------------------TGGGCA------------------------------ 1566

Qy         334 GlyAlaLeuCysMetGluLysSerLeuGlyProAsnSerCysSerAlaAsnGlyProGly 353
                                       :::|||   :::   |||         |||   |||
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Qy         354 LeuTyrLeuIleHisGlyProAsn 361
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Db        1609 GTGGGGTACAACCACCATGACAAC 1632

Search completed: June  8, 2004, 06:01:52
Job time : 109 secs
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                      GenCore version 5.1.6
           Copyright (c) 1993 - 2004  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         June  8, 2004, 18:54:10 ; Search time 829.5 Seconds
                                         (without alignments)
                                         16499.081 Million cell updates/sec

Title:          US-09-900-448-3_COPY_1_3000
Perfect score:  3000
Sequence:       1 tccctctccccaggcaggcc.........tggctgttcttcagtcctag 3000

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters:      5991872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES

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Result                Query
  No.      Score      Match  Length  DB  ID                         Description
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     1      3000      100.0   13737  11  US-09-900-448-3              Sequence 3, Appli
     2    1509.4       50.3    5234  15  US-10-311-455-917            Sequence 917, App
c    3    1281.6       42.7    5234  15  US-10-311-455-918            Sequence 918, App
     4       147        4.9     384  10  US-09-918-995-7738           Sequence 7738, Ap
     5       130        4.3     422  10  US-09-918-995-8595           Sequence 8595, Ap
     6       130        4.3     488  10  US-09-918-995-30828          Sequence 30828, A
     7       130        4.3    1631  15  US-10-125-237-19             Sequence 19, Appl
     8       130        4.3    1631  15  US-10-105-891-19             Sequence 19, Appl
     9       130        4.3    3186  11  US-09-900-448-1              Sequence 1, Appli
    10     128.4        4.3     492  10  US-09-918-995-31395          Sequence 31395, A
    11      94.8        3.2     225   9  US-09-960-352-3470           Sequence 3470, Ap
    12      94.8        3.2     237   9  US-09-960-352-7532           Sequence 7532, Ap
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    18      94.8        3.2     399   9  US-09-960-352-457            Sequence 457, App
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    23      94.8        3.2     407   9  US-09-960-352-6107           Sequence 6107, Ap
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    34        94        3.1     225   9  US-09-960-352-431            Sequence 431, App
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    39        93        3.1     861  16  US-10-162-335-87             Sequence 87, Appl
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    45      82.4        2.7    1516  15  US-10-316-253-39             Sequence 39, Appl


                                ALIGNMENTS


RESULT 1
US-09-900-448-3
; Sequence 3, Application US/09900448
; Publication No. US20030220488A1
; GENERAL INFORMATION:
;  APPLICANT: CECCARDI, Toni et al.
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001272
;  CURRENT APPLICATION NUMBER: US/09/900,448
;  CURRENT FILING DATE:  2001-07-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 13737
;   TYPE: DNA
;   ORGANISM: Human
US-09-900-448-3

  Query Match             100.0%;  Score 3000;  DB 11;  Length 13737;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3000;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCCTCTCCCCAGGCAGGCCCAGCAAAATCTGTAGGATTCAGACAGGTTCTGACAGCTG 60
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Qy         61 AAGACAAGTTGTTGAGGAAATTCCTGATGGAGGATCATGGGGTGCTCAGGAGGGAGAATA 120
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Qy       1921 TGGGGGTGGTGCTGCTGCCAACTCTATATAGGGAGTTCAACTGGTCACCCAGAGCTGTCC 1980
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Qy       2161 CAAATTTGGGGTCAGGGGCTATGGGAAAGGGATCGGTCCCAATGGATCAAGATATCTATT 2220
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Qy       2221 TTGTTCTCCCTAGGACTAGTGCCCATGGGAATGTTGCTGAAGGCGAGACCAAGCCAGACC 2280
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Db       2221 TTGTTCTCCCTAGGACTAGTGCCCATGGGAATGTTGCTGAAGGCGAGACCAAGCCAGACC 2280

Qy       2281 CAGACGTGACTGGTGAGGCCCTGACTCCCTAAGTCTGTCTTATCTGTCTGGTTGTGTCTC 2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CAGACGTGACTGGTGAGGCCCTGACTCCCTAAGTCTGTCTTATCTGTCTGGTTGTGTCTC 2340

Qy       2341 TGCATTTTATCACCTTCTGGTTTTTTTTTTTTTTTTTTTTTTTTACTTTGCCATCTCCCT 2400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TGCATTTTATCACCTTCTGGTTTTTTTTTTTTTTTTTTTTTTTTACTTTGCCATCTCCCT 2400
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Qy   2401 ACCTCCACCCCAGAACGCTGCTCAGATGGCTGGAGCTTTGATGCTACCACCCTGGATGAC 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ACCTCCACCCCAGAACGCTGCTCAGATGGCTGGAGCTTTGATGCTACCACCCTGGATGAC 2460

Qy   2461 AATGGAACCATGCTGTTTTTTAAAGGTAGGAGGGACTGAGGTTAGGGCGTTTAGGACCTT 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 AATGGAACCATGCTGTTTTTTAAAGGTAGGAGGGACTGAGGTTAGGGCGTTTAGGACCTT 2520

Qy   2521 AGACTTACTCTCCTTCACAAAGGGTGTCCCTGTCTGTGGGAGGTCTTAGGAATTATCTGA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 AGACTTACTCTCCTTCACAAAGGGTGTCCCTGTCTGTGGGAGGTCTTAGGAATTATCTGA 2580

Qy   2581 TGGTATCACTGACAGCTTCTCTCAAGCTATCTCAGTAGGTCAAAGGTTTCTCACTGGGCC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TGGTATCACTGACAGCTTCTCTCAAGCTATCTCAGTAGGTCAAAGGTTTCTCACTGGGCC 2640

Qy   2641 CCTCAGTGAGTGTGGGTTTTTTCAGGGGAGTTTGTGTGGAAGAGTCACAAATGGGACCGG 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 CCTCAGTGAGTGTGGGTTTTTTCAGGGGAGTTTGTGTGGAAGAGTCACAAATGGGACCGG 2700

Qy   2701 GAGTTAATCTCAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAA 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GAGTTAATCTCAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAA 2760

Qy   2761 GGTCACAACAGTGTCTTTCTGATCAAGGTACTGCTGGGCCAAAATCAGGGCCAGGCTGGA 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 GGTCACAACAGTGTCTTTCTGATCAAGGTACTGCTGGGCCAAAATCAGGGCCAGGCTGGA 2820

Qy   2821 AAGGGCTGGAATCGACACTGGGGACCCTTCCCCCAAATGGCCTTGGCATGGAGCCCATAG 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AAGGGCTGGAATCGACACTGGGGACCCTTCCCCCAAATGGCCTTGGCATGGAGCCCATAG 2880

Qy   2881 CAATAGGTAGCAGATTTCTTTCCCATGTGCCCTCCTTTCCTGTAAAAGCTTGGGCTAAGG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CAATAGGTAGCAGATTTCTTTCCCATGTGCCCTCCTTTCCTGTAAAAGCTTGGGCTAAGG 2940

Qy   2941 GAGTGTGCATGCGTGTGGGCCTGGCAGGTGCACCATCCAGTGGCTGTTCTTCAGTCCTAG 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 GAGTGTGCATGCGTGTGGGCCTGGCAGGTGCACCATCCAGTGGCTGTTCTTCAGTCCTAG 3000


RESULT 2
US-10-311-455-917
; Sequence 917, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
;  TITLE OF INVENTION:  cytosine methylation
;  FILE REFERENCE: 5013.1014
;  CURRENT APPLICATION NUMBER: US/10/311,455
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: PCT/EP01/07537
;  PRIOR FILING DATE: 2001-07-02
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 917
;   LENGTH: 5234
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-917

  Query Match             50.3%;  Score 1509.4;  DB 15;  Length 5234;
  Best Local Similarity   79.9%;  Pred. No. 0;
  Matches 1777;  Conservative    0;  Mismatches  446;  Indels    0;  Gaps    0;
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Qy     12 AGGCAGGCCCAGCAAAATCTGTAGGATTCAGACAGGGTTCTGACAGCTGAAGACAAGTTG 71
          ||| |||   || ||||| ||||||||| ||| |||||| ||| || |||||| ||||||
Db   3012 AGGTAGGTTTAGTAAAATTTGTAGGATTTAGATAGGGTTTTGATAGTTGAAGATAAGTTG 3071

Qy     72 TTGAGGAAATTCCTGATGGAGGATCATGGGGTGCTCAGGAGGGAGAATATAAGGTTTCAG 131
          |||||||||||  ||||||||||| |||||||| | ||||||||||||||||||||| ||
Db   3072 TTGAGGAAATTTTTGATGGAGGATTATGGGGTGTTTAGGAGGGAGAATATAAGGTTTTAG 3131

Qy    132 AGGCTGAGAGGGAAAGAAAAGGTGAGGGGGAGTCTTAGAATAGTGGCTCCCATTGCCCAA 191
          ||| ||||||||||||||||||||||||||||| |||||||||||| |   ||||   ||
Db   3132 AGGTTGAGAGGGAAAGAAAAGGTGAGGGGGAGTTTTAGAATAGTGGTTTTTATTGTTTAA 3191

Qy    192 CACCCAGAAAGAAGACATGCCCTGCAATGGGGAGAAGGTGAGTATGAGACATTGGCTGTA 251
           |   |||||||||| |||   || |||||||||||||||||||||||| ||||| ||||
Db   3192 TATTTAGAAAGAAGATATGTTTTGTAATGGGGAGAAGGTGAGTATGAGATATTGGTTGTA 3251

Qy    252 GCAGCGATGGCATTGCCCAGGCTGCCAAGGACTCAGAGAGTCCAGCCTTGCCCACTGACC 311
          | |||||||| ||||   ||| ||  ||||| | |||||||  ||  |||   | |||  
Db   3252 GTAGCGATGGTATTGTTTAGGTTGTTAAGGATTTAGAGAGTTTAGTTTTGTTTATTGATT 3311

Qy    312 TATGAGGAGGGAATGATGTTCACAGCACATTTTCATTCGTAAGTCAGGAGAGGACATTGA 371
          |||||||||||||||||||| | || | ||||| |||||||||| ||||||||| |||||
Db   3312 TATGAGGAGGGAATGATGTTTATAGTATATTTTTATTCGTAAGTTAGGAGAGGATATTGA 3371

Qy    372 GCCTGATGGCAGAGGCCTGGTGACATGTTGTTCCAGAGGTTCCGGAATGTGTGTTTTCCT 431
          |  |||||| |||||  |||||| ||||||||  ||||||| |||||||||||||||  |
Db   3372 GTTTGATGGTAGAGGTTTGGTGATATGTTGTTTTAGAGGTTTCGGAATGTGTGTTTTTTT 3431

Qy    432 GTTGGAAGGAAACTTCGCAGAGTAGAAAAGGGATCTGAGACTTTTGGTAAGATTATATAT 491
          |||||||||||| |||| |||||||||||||||| ||||| |||||||||||||||||||
Db   3432 GTTGGAAGGAAATTTCGTAGAGTAGAAAAGGGATTTGAGATTTTTGGTAAGATTATATAT 3491

Qy    492 GGGACTGTCAGGGGTCTGGAGCCATCTGTGAGGGATCAGGGCCCTTTCAGCCTTGGCTAG 551
          |||| ||| |||||| |||||  || |||||||||| ||||   ||| ||  |||| |||
Db   3492 GGGATTGTTAGGGGTTTGGAGTTATTTGTGAGGGATTAGGGTTTTTTTAGTTTTGGTTAG 3551

Qy    552 GGAGCAGGGGTCCTGGAACTTCATCCTGGCCCATAGCTGAGTCTGCCCATAATTCTTTTC 611
          |||| ||||||  ||||| || ||  |||   |||| ||||| ||   |||||| |||| 
Db   3552 GGAGTAGGGGTTTTGGAATTTTATTTTGGTTTATAGTTGAGTTTGTTTATAATTTTTTTT 3611

Qy    612 TGACTCACTAGGCAAATCTCACACAGAAATGGGGCAGCTTTGGGAGTGGGCCCAGGAAGT 671
          ||| | | |||| |||| | | | |||||||||| || ||||||||||||   |||||||
Db   3612 TGATTTATTAGGTAAATTTTATATAGAAATGGGGTAGTTTTGGGAGTGGGTTTAGGAAGT 3671

Qy    672 ACTGAGGATAGCAGGTGAGATCCCAGGAAGAGATGGATGTGGGGCCGAGACACTGGAGAG 731
          | ||||||||| |||||||||   |||||||||||||||||||| ||||| | |||||||
Db   3672 ATTGAGGATAGTAGGTGAGATTTTAGGAAGAGATGGATGTGGGGTCGAGATATTGGAGAG 3731

Qy    732 AGAAACAGGACTGTCAGATAAAGGGCGTCTGTGACTCCTAGATCTCATTATGCCTACTAC 791
          ||||| |||| ||| ||||||||||||| ||||| |  ||||| | ||||||  || || 
Db   3732 AGAAATAGGATTGTTAGATAAAGGGCGTTTGTGATTTTTAGATTTTATTATGTTTATTAT 3791

Qy    792 CATAACCTACCCCCAATTCCTAATATTCTCCTACCCTAGAGGGGGGGAAATTGTCAGAAA 851
           ||||  ||     ||||  ||||||| |  ||   |||||||||||||||||| |||||
Db   3792 TATAATTTATTTTTAATTTTTAATATTTTTTTATTTTAGAGGGGGGGAAATTGTTAGAAA 3851

Qy    852 TTTGGCTGCAACACTAGCAACACTACTCAGTACTTGAAATGCATTTTTGCATTTTTTTCA 911
          ||||| || || | ||| || | || | |||| |||||||| ||||||| |||||||| |
Db   3852 TTTGGTTGTAATATTAGTAATATTATTTAGTATTTGAAATGTATTTTTGTATTTTTTTTA 3911

Qy    912 TTCAACAAATATTTCTGGAACAACTCTTATATGCCAGGCACTATTTTAGGAGTCAGGGAT 971
          || || |||||||| ||||| || | |||||||  ||| | |||||||||||| ||||||
Db   3912 TTTAATAAATATTTTTGGAATAATTTTTATATGTTAGGTATTATTTTAGGAGTTAGGGAT 3971

Qy    972 ATATAATGGTAAACAAGACAGGCAAAACAAAGCAAAGCAACAACAACCATCACCAGATAA 1031
          ||||||||||||| |||| ||| |||| |||| |||| || || ||  || |  ||||||
Db   3972 ATATAATGGTAAATAAGATAGGTAAAATAAAGTAAAGTAATAATAATTATTATTAGATAA 4031

Qy   1032 GTAGACAGATGAAAGAATTTCAAGTTTTAGTAAGTAAAATAAAACAAGCAAGGGTCTGAA 1091
          ||||| |||||||||||||| ||||||||||||||||||||||| ||| |||||| ||||
Db   4032 GTAGATAGATGAAAGAATTTTAAGTTTTAGTAAGTAAAATAAAATAAGTAAGGGTTTGAA 4091
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Qy        1092 ATGGCTAGATAAGGCGGTCAAGAAAGGCTTCATTGAGAAGGTAGCATTTAAGCAGGAGTC 1151
               |||| ||||||||| ||| |||||||| || |||||||||||||| |||||||| ||||||
Db        4092 ATGGTTAGATAAGGTGGTTAAGAAAGGTTTTATTGAGAAGGTAGTATTTAAGTAGGAGTT 4151

Qy        1152 AGCTAGAAATATTGTGAAATTCCAGTTACAGTTCTATTTGTTCTGGGTTGGTTAAATAAA 1211
               || |||||||||||||||||||  ||||| ||||| |||||||| ||||||||||||||||||
Db        4152 AGTTAGAAATATTGTGAAATTTTAGTTATAGTTTTATTTGTTTTGGGTTGGTTAAATAAA 4211

Qy        1212 GCTTTTTCCCCCAAGGTGGAAACTACCAAGAAAGACTAATTACTAGTAGTGGTGGTGCTC 1271
               | |||||     ||||||||||| ||  |||||||| |||||| ||||||||||||||| | 
Db        4212 GTTTTTTTTTTTAAGGTGGAAATTATTAAGAAAGATTAATTATTAGTAGTGGTGGTGTTT 4271

Qy        1272 TCTGGAAGAGAGACACCTCCTGTTTCTGCCTCATTACTGTCAACCCTTCACTTCCAGGCA 1331
               | |||||||||||| |  |  ||||| ||  | |||| ||| ||   || | ||  ||| |
Db        4272 TTTGGAAGAGAGATATTTTTTGTTTTTGTTTTATTATTGTTAATTTTTTATTTTTAGGTA 4331

Qy        1332 CTTTTTGCAAAGCCCTTTGCCAGTCAGGGAAGGCGAGAGGCTGGGCATGGGGCTTGGACA 1391
                |||||| |||||   |||| ||| ||||||||||||||||| |||| |||||| ||||| |
Db        4332 TTTTTTGTAAAGTTTTTTGTTAGTTAGGGAAGGCGAGAGGTTGGGTATGGGGTTTGGATA 4391

Qy        1392 TTTGACAACAGTGAGACATTATTGTCCCCAGACTCACTAGCCCAAGGGTAAAGCTGAAGA 1451
               ||||| || ||||||| ||||||||    ||| | | |||   |||||||||| ||||||
Db        4392 TTTGATAATAGTGAGATATTATTGTTTTTAGATTTATTAGTTTAAGGGTAAAGTTGAAGA 4451

Qy        1452 GGCTTGGGCATGCCCCAGAAAGGCCCCTGATGAAGCTTGGAAAAAGCTGTTCTCTGAGTA 1511
               || ||||| |||    |||||||    |||||||| |||||||||| ||||| | ||||||
Db        4452 GGTTTGGGTATGTTTTAGAAAGGTTTTTGATGAAGTTTGGAAAAAGTTGTTTTTTGAGTA 4511

Qy        1512 TTTCTAAGTAAGTTTATCTGTGTGTGTGGTTACTAAAAGTAGTAAGTATTGCTGTCTCTA 1571
               ||| ||||||||||||| |||||||||||||| ||||||||||||||||||| ||| | ||
Db        4512 TTTTTAAGTAAGTTTATTTGTGTGTGTGGTTATTAAAAGTAGTAAGTATTGTTGTTTTTA 4571

Qy        1572 GCTGCCTTAGAGCAGGGCTTGACACAGTACACAGCAATATTAGTTCCCTCCTTTTCTCAC 1631
               | ||  |||||| |||| |||| | |||| | || |||||||||||   |  |||| | | 
Db        4572 GTTGTTTTAGAGTAGGGTTTGATATAGTATATAGTAATATTAGTTTTTTTTTTTTTTTAT 4631

Qy        1632 CTCCCCCATTGTGGAGATAAACTCAATCACAAAAGGTGATCCTCAGTCTACTCACTTCCC 1691
                |     |||||||||||||| | ||| | |||||||||||  | ||| || | ||   
Db        4632 TTTTTTTATTGTGGAGATAAATTTAATTATAAAAGGTGATTTTTAGTTTATTTATTTTTT 4691

Qy        1692 TGACTTATGGATGCCTGGACCCATTGCCAGTGTGAGAGTCACAGCTGGACGTCAGCAGTG 1751
               ||| ||||||||||  ||||   ||||  |||||||||||| | || ||||||| || ||||
Db        4692 TGATTTATGGATGTTTGGATTTATTGTTAGTGTGAGAGTTATAGTTGGACGTTAGTAGTG 4751

Qy        1752 TAGCCCAGTTACTGCTTGAAAATTGCTGAAGGGGGTTGGGGGGCAGCTGCCGGGAAAAAG 1811
               |||   |||||| || |||||||||| |||||||||||||||||||| || || ||||||||||
Db        4752 TAGTTTAGTTATTGTTTGAAAATTGTTGAAGGGGGTTGGGGGGTAGTTGTCGGGAAAAAG 4811

Qy        1812 GAGTCTTGGATTCAGATTTCTGTCCAGACCCTGACCTTATTTGCAGTGATGTAATCAGCC 1871
               |||| ||||||| ||||||| |||  |||   |||  ||||||| ||||||||||| ||  
Db        4812 GAGTTTTGGATTTAGATTTTTGTTTAGATTTTGATTTTATTTGTAGTGATGTAATTAGTT 4871

Qy        1872 AATATTGGCTTAGTCCTGGGAGACAGCACATTCCCAGTAGAGTTGGAGGTGGGGGTGGTG 1931
               |||||||| |||||  |||||||| || | |||   ||||||||||||||||||||||||||||
Db        4872 AATATTGGTTTAGTTTTGGGAGATAGTATATTTTTAGTAGAGTTGGAGGTGGGGGTGGTG 4931

Qy        1932 CTGCTGCCAACTCTATATAGGGAGTTCAACTGGTCACCCAGAGCTGTCCTGTGGCCTCTG 1991
                || ||  || | |||||||||||||| || |||| |   |||| |||  ||||||  | ||
Db        4932 TTGTTGTTAATTTTATATAGGGAGTTTAATTGGTTATTTAGAGTTGTTTTGTGGTTTTTG 4991

Qy        1992 CAGCTCAGCATGGCTAGGGTACTGGGAGCACCCGTTGCACTGGGGTTGTGGAGCCTATGC 2051
                || | || |||| |||||| |||||| |  ||||| | ||||||||||||||  ||||  
Db        4992 TAGTTTAGTATGGTTAGGGTATTGGGAGTATTCGTTGTATTGGGGTTGTGGAGTTTATGT 5051

Qy        2052 TGGTCTCTGGCCATTGCCACCCCTCTTCCTCCGTGAGTAAAGCTGGGACTAGAAGCGAAG 2111
               |||| | |||  ||||  |    | ||  | ||||||||||||| ||||| ||||||||||||
Db        5052 TGGTTTTTGGTTATTGTTATTTTTTTTTTTCGTGAGTAAAGTTGGGATTAGAAGCGAAG 5111

Qy        2112 GATTGAGTTCTGGGCTAGGGTAAGGTAGGGCCAGTTTTTAGGCCTCGGTCAAATTTGGGG 2171
               ||||||||| |||| |||||||||||||||||  ||||||||||||  ||||| ||||||||||
Db        5112 GATTGAGTTTTGGGTTAGGGTAAGGTAGGGTTAGTTTTTAGGTTTCGGTTAAATTTGGGG 5171

Qy        2172 TCAGGGGCTATGGGAAAGGGATCGGTCCCAATGGATCAAGATATCTATTTTGTTCTCCCT 2231
               | ||||| ||||||||||||||||||   ||||||| |||||||| ||||||||| |   |
Db        5172 TTAGGGGTTATGGGAAAGGGATCGGTTTTAATGGATTAAGATATTTATTTTGTTTTTTTT 5231

Qy        2232 AGG 2234
               |||
Db        5232 AGG 5234


RESULT 3
US-10-311-455-918/c
; Sequence 918, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
;  TITLE OF INVENTION:  cytosine methylation
;  FILE REFERENCE: 5013.1014
;  CURRENT APPLICATION NUMBER: US/10/311,455
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: PCT/EP01/07537
;  PRIOR FILING DATE: 2001-07-02
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 918
;   LENGTH: 5234
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-918

  Query Match             42.7%;  Score 1281.6;  DB 15;  Length 5234;
  Best Local Similarity   73.4%;  Pred. No. 0;
  Matches 1638;  Conservative    0;  Mismatches  594;  Indels    0;  Gaps    0;

Qy           1 TCCCTCTCCCCAGGCAGGCCCAGCAAAATCTGTAGGATTCAGACAGGGTTCTGACAGCTG 60
               ||||||||||||  ||  |||| |||||||| ||  ||||| |||   |||| ||| ||
Db        2234 TCCCTCTCCCCAAACAAACCCAACAAAATCTATAAAATTCAAACAAAATTCTAACAACTA 2175

Qy          61 AAGACAAGTTGTTGAGGAAATTCCTGATGGAGGATCATGGGGTGCTCAGGAGGGAGAATA 120
               || |||| || || |  |||||||| ||  |  |||||    | ||||  |   | ||||
Db        2174 AAAACAAATTATTAAAAAAATTCCTAATAAAAAATCATAAAATACTCAAAAAAAAAAATA 2115

Qy         121 TAAGGTTTCAGAGGCTGAGAGGGAAAGAAAAGGTGAGGGGGAGTCTTAGAATAGTGGCTC 180
               |||  ||||| |  || | |   ||| ||||  | |     | ||||| ||||| |  |||
Db        2114 TAAAATTTCAAAAACTAAAAAAAAAAAAAAAAATAAAAAAAAATCTTAAAATAATAACTC 2055

Qy         181 CCATTGCCCAACACCCAGAAAGAAGACATGCCCTGCAATGGGGAGAAGGTGAGTATGAGA 240
               ||||| ||||||||||||| ||| || |||| |||| ||||    | ||  | | ||| | |
Db        2054 CCATTACCCAACACCCAAAAAAAAAACATACCCTACAATAAAAAAAAATAAATATAAAA 1995

Qy         241 CATTGGCTGTAGCAGCGATGGCATTGCCCAGGCTGCCAAGGACTCAGAGAGTCCAGCCTT 300
               ||||  || || || |||| |||| ||||  || ||||  ||||| | | |||| ||||
Db        1994 CATTAACTATAACAACGATAACATTACCCAAACTACCAAAAACTCAAAAAATCCAACCTT 1935

Qy         301 GCCCACTGACCTATGAGGAGGGAATGATGTTCACAGCACATTTTCATTCGTAAGTCAGGA 360
                |||||| ||||||| |  |   ||| || ||||||| |||||||||||||||||| ||   |
Db        1934 ACCCACTAACCTATAAAAAAAAAATAATATTCACAACACATTTTCATTCGTAAATCAAAA 1875

Qy         361 GAGGACATTGAGCCTGATGGCAGAGGCCTGGTGACATGTTGTTCCAGAGGTTCCGGAATG 420
                |  ||||| | ||| ||  || |  |||  | |||| || ||||| |  ||||| |||
Db        1874 AAAAACATTAAACCTAATAACAAAAACCTAATAACATATTATTCCAAAAATTCCGAAATA 1815

Qy         421 TGTGTTTTCCTGTTGGAAGGAAACTTCGCAGAGTAGAAAAGGGATCTGAGACTTTTGGTA 480
               | | |||||| | ||  ||  |||||||||| | || ||||   |||| | ||||||  ||
Db        1814 TATATTTTCCTATTAAAAAAAAACTTCGCAAAATAAAAAAAAAATCTAAAACTTTTAATA 1755

Qy         481 AGATTATATATGGGACTGTCAGGGGTCTGGAGCCATCTGTGAGGATCAGGGCCCTTTCA 540
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Db       1754 AAATTATATATAAAACTATCAAAAATCTAAAACCATCTATAAAAAATCAAAACCCTTTCA 1695

Qy        541 GCCTTGGCTAGGGAGCAGGGGTCCTGGAACTTCATCCTGGCCCATAGCTGAGTCTGCCCA 600

Db       1694 ACCTTAACTAAAAAACAAAAATCCTAAAACTTCATCCTAACCCATAACTAAATCTACCCA 1635

Qy        601 TAATTCTTTTCTGACTCACTAGGCAAATCTCACACAGAAATGGGGCAGCTTTGGGAGTGG 660

Db       1634 TAATTCTTTTCTAACTCACTAAACAAATCTCACACAAAAATAAAACAACTTTAAAAATAA 1575

Qy        661 GCCCAGGAAGTACTGAGGATAGCAGGTGAGATCCCAGGAAGAGATGGATGTGGGGCCGAG 720

Db       1574 ACCCAAAAAATACTAAAAATAACAAATAAAATCCCAAAAAAAAATAAATATAAAACCGAA 1515

Qy        721 ACACTGGAGAGAGAAACAGGACTGTCAGATAAAGGGCGTCTGTGACTCCTAGATCTCATT 780

Db       1514 ACACTAAAAAAAAAAACAAAACTATCAAATAAAAAACGTCTATAACTCCTAAATCTCATT 1455

Qy        781 ATGCCTACTACCATAACCTACCCCCAATTCCTAATATTCTCCTACCCTAGAGGGGGGGAA 840

Db       1454 ATACCTACTACCATAACCTACCCCCAATTCCTAATATTCTCCTACCCTAAAAAAAAAAAA 1395

Qy        841 ATTGTCAGAAATTTGGCTGCAACACTAGCAACACTACTCAGTACTTGAAATGCATTTTTG 900

Db       1394 ATTATCAAAAATTTAACTACAACACTAACAACACTACTCAATACTTAAAATACATTTTTA 1335

Qy        901 CATTTTTTTCATTCAACAAATATTTCTGGAACAACTCTTATATGCCAGGCACTATTTTAG 960

Db       1334 CATTTTTTTCATTCAACAAATATTTCTAAAACAACTCTTATATACCAAACACTATTTTAA 1275

Qy        961 GAGTCAGGGATATATAATGGTAAACAAGACAGGCAAAACAAAGCAAAGCAACAACAACCA 1020

Db       1274 AAATCAAAAATATATAATAATAAACAAAACAAACAAAACAAAACAAAACAACAACAACCA 1215

Qy       1021 TCACCAGATAAGTAGACAGATGAAAGAATTTCAAGTTTTAGTAAGTAAAATAAAACAAGC 1080

Db       1214 TCACCAAATAAATAAACAAATAAAAAAATTTCAAATTTTAATAAATAAAATAAAACAAAC 1155

Qy       1081 AAGGGTCTGAAATGGCTAGATAAGGCGGTCAAGAAAGGCTTCATTGAGAAGGTAGCATTT 1140

Db       1154 AAAAATCTAAAATAACTAAATAAAATAATCAAAAAAAACTTCATTAAAAAAATAACATTT 1095

Qy       1141 AAGCAGGAGTCAGCTAGAAATATTGTGAAATTCCAGTTACAGTTCTATTTGTTCTGGGTT 1200

Db       1094 AAACAAAAATCAACTAAAAATATTATAAAATTCCAATTACAATTCTATTTATTCTAAATT 1035

Qy       1201 GGTTAAATAAAGCTTTTTCCCCCAAGGTGGAAACTACCAAGAAAGACTAATTACTAGTAG 1260

Db       1034 AATTAAATAAAACTTTTTCCCCCAAAATAAAAACTACCAAAAAAAACTAATTACTAATAA 975

Qy       1261 TGGTGGTGCTCTCTGGAAGAGAGACACCTCCTGTTTCTGCCTCATTACTGTCAACCCTTC 1320

Db        974 TAATAATACTCTCTAAAAAAAAAACACCTCCTATTTCTACCTCATTACTATCAACCCTTC 915

Qy       1321 ACTTCCAGGCACTTTTTGCAAAGCCCTTTGCCAGTCAGGGAAGGCGAGAGGCTGGGCATG 1380

Db        914 ACTTCCAAACACTTTTTACAAAACCCTTTACCAATCAAAAAAAACGAAAAACTAAACATA 855

Qy       1381 GGGCTTGGACATTTGACAACAGTGAGACATTATTGTCCCCAGACTCACTAGCCCAAGGGT 1440

Db        854 AAACTTAAACATTTAACAACAATAAAACATTATTATCCCCAAACTCACTAACCCAAAAAT 795

Qy       1441 AAAGCTGAAGAGGCTTGGGCATGCCCCAGAAAGGCCCCTGATGAAGCTTGGAAAAAGCTG 1500

Db        794 AAAACTAAAAAAACTTAAACATACCCCAAAAAAACCCCTAATAAAACTTAAAAAAAACTA 735

Qy       1501 TTCTCTGAGTATTTCTAAGTAAGTTTATCTGTGTGTGTGGTTACTAAAAGTAGTAAGTAT 1560

Db        734 TTCTCTAAATATTTCTAAATAAATTTATCTATATATATAATTACTAAAAATAATAAATAT 675

Qy       1561 TGCTGTCTCTAGCTGCCTTAGAGCAGGGCTTGACACAGTACACAGCAATATTAGTTCCCT 1620

Db        674 TACTATCTCTAACTACCTTAAAACAAAACTTAACACAATACACAACAATATTAATTCCCT 615

Qy       1621 CCTTTTCTCACCTCCCCCATTGTGGAGATAAACTCAATCACAAAAGGTGATCCTCAGTCT 1680

Db        614 CCTTTTCTCACCTCCCCCATTATAAAAATAAACTCAATCACAAAAAATAATCCTCAATCT 555

Qy       1681 ACTCACTTCCCTGACTTATGGATGCCTGGACCCATTGCCAGTGTGAGAGTCACAGCTGGA 1740

Db        554 ACTCACTTCCCTAACTTATAAATACCTAAACCCATTACCAATATAAAAATCACAACTAAA 495

Qy       1741 CGTCAGCAGTGTAGCCCAGTTACTGCTTGAAAATTGCTGAAGGGGGTTGGGGGGCAGCTG 1800

Db        494 CGTCAACAATATAACCCAATTACTACTTAAAAATTACTAAAAAAAATTAAAAAACAACTA 435

Qy       1801 CCGGGAAAAAGGAGTCTTGGATTCAGATTTCTGTCCAGACCCTGACCTTATTTGCAGTGA 1860

Db        434 CCGAAAAAAAAAAATCTTAAATTCAAATTTCTATCCAAACCCTAACCTTATTTACAATAA 375

Qy       1861 TGTAATCAGCCAATATTGGCTTAGTCCTGGGAGACAGCACATTCCCAGTAGAGTTGGAGG 1920

Db        374 TATAATCAACCAATATTAACTTAATCCTAAAAAACAACACATTCCCAATAAAATTAAAAA 315

Qy       1921 TGGGGGTGGTGCTGCTGCCAACTCTATATAGGGAGTTCAACTGGTCACCCAGAGCTGTCC 1980

Db        314 TAAAAATAATACTACTACCAACTCTATATAAAAAATTCAACTAATCACCCAAAACTATCC 255

Qy       1981 TGTGGCCTCTGCAGCTCAGCATGGCTAGGGTACTGGGAGCACCCGTTGCACTGGGGTTGT 2040

Db        254 TATAACCTCTACAACTCAACATAACTAAAATACTAAAAACACCCGTTACACTAAAATTAT 195

Qy       2041 GGAGCCTATGCTGGTCTCTGGCCATTGCCACCCCTCTTCCTCCGTGAGTAAAGCTGGGAC 2100

Db        194 AAAACCTATACTAATCTCTAACCATTACCACCCCTCTTCCTCCGTAAATAAAACTAAAAC 135

Qy       2101 TAGAAGCGAAGGATTGAGTTCTGGGCTAGGGTAAGGTAGGGCCAGTTTTTAGGCCTCGGT 2160

Db        134 TAAAAACGAAAAATTAAATTCTAAACTAAAATAAAATAAAACCAATTTTTAAACCTCGAT 75

Qy       2161 CAAATTTGGGGTCAGGGGCTATGGGAAAGGGATCGGTCCCAATGGATCAAGATATCTATT 2220

Db         74 CAAATTTAAAATCAAAAACTATAAAAAAAAAATCGATCCCAATAAATCAAAATATCTATT 15

Qy       2221 TTGTTCTCCCTA 2232

Db         14 TTATTCTCCCTA 3


RESULT 4
US-09-918-995-7738
; Sequence 7738, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7738
;   LENGTH: 384
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-918-995-7738

  Query Match             4.9%;  Score 147;  DB 10;  Length 384;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-32;
  Matches  147;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1985 GCCTCTGCAGCTCAGCATGGCTAGGGTACTGGGAGCACCCGTTGCACTGGGGTTGTGGAG 2044
```

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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GCCTCTGCAGCTCAGCATGGCTAGGGTACTGGGAGCACCCGTTGCACTGGGGTTGTGGAG 60

Qy        2045 CCTATGCTGGTCTCTGGCCATTGCCACCCCTCTTCCTCCGTGAGTAAAGCTGGGACTAGA 2104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 CCTATGCTGGTCTCTGGCCATTGCCACCCCTCTTCCTCCGTGAGTAAAGCTGGGACTAGA 120

Qy        2105 AGCGAAGGATTGAGTTCTGGGCTAGGG 2131
               |||||||||||||||||||||||||||
Db         121 AGCGAAGGATTGAGTTCTGGGCTAGGG 147


RESULT 5
US-09-918-995-8595
; Sequence 8595, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8595
;   LENGTH: 422
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-918-995-8595

  Query Match             4.3%;  Score 130;  DB 10;  Length 422;
  Best Local Similarity   96.4%;  Pred. No. 3.1e-27;
  Matches  133;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        2651 TGTGGGTTTTTTTCAGGGGAGTTTGTGTGGAAGAGTCACAAATGGACCGGGAGTTAATCT 2710
               ||  | ||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db         213 TGCTGTTTTTTTAAAGGGGAGTTTGTGTGGAAGAGTCACAAATGGACCGGGAGTTAATCT 272

Qy        2711 CAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAAGGTCACAACA 2770
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         273 CAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAAGGTCACAACA 332

Qy        2771 GTGTCTTTCTGATCAAGG 2788
               ||||||||||||||||||
Db         333 GTGTCTTTCTGATCAAGG 350


RESULT 6
US-09-918-995-30828
; Sequence 30828, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 30828
;   LENGTH: 488
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(488)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-30828

  Query Match             4.3%;  Score 130;  DB 10;  Length 488;
  Best Local Similarity   96.4%;  Pred. No. 3.5e-27;
  Matches  133;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        2651 TGTGGGTTTTTTTCAGGGGAGTTTGTGTGGAAGAGTCACAAATGGACCGGGAGTTAATCT 2710
               ||  | ||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db         270 TGCTGTTTTTTTAAAGGGGAGTTTGTGTGGAAGAGTCACAAATGGACCGGGAGTTAATCT 329

Qy        2711 CAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAAGGTCACAACA 2770
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         330 CAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAAGGTCACAACA 389

Qy        2771 GTGTCTTTCTGATCAAGG 2788
               ||||||||||||||||||
Db         390 GTGTCTTTCTGATCAAGG 407


RESULT 7
US-10-125-237-19
; Sequence 19, Application US/10125237
; Publication No. US20030022329A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: No. US20030022329A1el Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 791CIP2ADIV
;  CURRENT APPLICATION NUMBER: US/10/125,237
;  CURRENT FILING DATE:  2002-04-17
;  PRIOR APPLICATION NUMBER: 09/668,317
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: 09/552,929
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 91
;  SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 19
;   LENGTH: 1631
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (71)..(1459)
US-10-125-237-19

  Query Match             4.3%;  Score 130;  DB 15;  Length 1631;
  Best Local Similarity   96.4%;  Pred. No. 8.1e-27;
  Matches  133;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        2651 TGTGGGTTTTTTTCAGGGGAGTTTGTGTGGAAGAGTCACAAATGGACCGGGAGTTAATCT 2710
               ||  | ||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db         270 TGCTGTTTTTTTAAAGGGGAGTTTGTGTGGAAGAGTCACAAATGGACCGGGAGTTAATCT 329

Qy        2711 CAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAAGGTCACAACA 2770
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         330 CAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAAGGTCACAACA 389

Qy        2771 GTGTCTTTCTGATCAAGG 2788
               ||||||||||||||||||
Db         390 GTGTCTTTCTGATCAAGG 407


RESULT 8
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```
US-10-105-891-19
; Sequence 19, Application US/10105891
; Publication No. US20030073099A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: No. US20030073099A1el Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 791CIP2A
;  CURRENT APPLICATION NUMBER: US/10/105,891
;  CURRENT FILING DATE:  2002-03-25
;  PRIOR APPLICATION NUMBER: 09/668,317
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: 09/552,929
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 91
;  SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 19
;   LENGTH: 1631
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (71)..(1459)
US-10-105-891-19

  Query Match             4.3%;  Score 130;  DB 15;  Length 1631;
  Best Local Similarity   96.4%;  Pred. No. 8.1e-27;
  Matches  133;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2651 TGTGGGTTTTTTCAGGGGAGTTTGTGTGGAAGAGTCACAAATGGACCGGGAGTTAATCT 2710
              ||  | |||||  |||||||||||||||||||||||||||||||||||||||||||||||
Db        270 TGCTGTTTTTTAAAGGGGAGTTTGTGTGGAAGAGTCACAAATGGACCGGGAGTTAATCT 329

Qy       2711 CAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAAGGTCACAACA 2770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 CAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAAGGTCACAACA 389

Qy       2771 GTGTCTTTCTGATCAAGG 2788
              ||||||||||||||||||
Db        390 GTGTCTTTCTGATCAAGG 407

RESULT 9
US-09-900-448-1
; Sequence 1, Application US/09900448
; Publication No. US20030220488A1
; GENERAL INFORMATION:
;  APPLICANT: CECCARDI, Toni et al.
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001272
;  CURRENT APPLICATION NUMBER: US/09/900,448
;  CURRENT FILING DATE:  2001-07-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 3186
;   TYPE: DNA
;   ORGANISM: Human
US-09-900-448-1

  Query Match             4.3%;  Score 130;  DB 11;  Length 3186;
  Best Local Similarity   96.4%;  Pred. No. 1.3e-26;
  Matches  133;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2651 TGTGGGTTTTTTCAGGGGAGTTTGTGTGGAAGAGTCACAAATGGACCGGGAGTTAATCT 2710
              ||  | |||||  |||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TGCTGTTTTTTAAAGGGGAGTTTGTGTGGAAGAGTCACAAATGGACCGGGAGTTAATCT 273

Qy       2711 CAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAAGGTCACAACA 2770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 CAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAAGGTCACAACA 333

Qy       2771 GTGTCTTTCTGATCAAGG 2788
              ||||||||||||||||||
Db        334 GTGTCTTTCTGATCAAGG 351

RESULT 10
US-09-918-995-31395
; Sequence 31395, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31395
;   LENGTH: 492
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(492)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31395

  Query Match             4.3%;  Score 128.4;  DB 10;  Length 492;
  Best Local Similarity   95.7%;  Pred. No. 1e-26;
  Matches  132;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2651 TGTGGGTTTTTTCAGGGGAGTTTGTGTGGAAGAGTCACAAATGGACCGGGAGTTAATCT 2710
              ||  | |||||  |||||||||||||||||||||||||||||||||||||||||||||||
Db        255 TGCTGTTTTTTAAAGGGGAGTTTGTGTGGAAGAGTCACAAATGGACCGGGAGTTAATCT 314

Qy       2711 CAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAAGGTCACAACA 2770
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 CACAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAAGGTCACAACA 374

Qy       2771 GTGTCTTTCTGATCAAGG 2788
              ||||||||||||||||||
Db        375 GTGTCTTTCTGATCAAGG 392

RESULT 11
US-09-960-352-3470
; Sequence 3470, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 3470
;   LENGTH: 225
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 15-LIB34-057-Q1-E1-D11
US-09-960-352-3470

  Query Match             3.2%;  Score 94.8;  DB 9;  Length 225;
  Best Local Similarity   80.4%;  Pred. No. 5.2e-17;
  Matches  111;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy       2651 TGTGGGTTTTTTCAGGGGAGTTTGTGTGGAAGAGTCACAAATGGGACCGGGAGTTAATCT 2710
              ||  | ||||   ||||||||||||||||||| ||||    |||| |||| |||| ||||
Db         38 TGCTGTTTTTAAAAGGGGAGTTTGTGTGGAAGGGTCATGCCTGGGCCCGGCAGTTGATCT 97

Qy       2711 CAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAAGGTCACAACA 2770
              ||||||| |||||| ||  |||||| || |||||||||||||||||  | | ||  ||||
Db         98 CAGAGAGGTGGAAGGATGCCCCCAGTCCCGTGGATGCTGCATTCCGCTATGATCGTAACA 157

Qy       2771 GTGTCTTTCTGATCAAGG 2788
              ||||| ||||||||||||
Db        158 GTGTCCTTCTGATCAAGG 175


RESULT 12
US-09-960-352-7532
; Sequence 7532, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 7532
;   LENGTH: 237
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 32-LIB34-054-Q1-E1-H7
US-09-960-352-7532

  Query Match             3.2%;  Score 94.8;  DB 9;  Length 237;
  Best Local Similarity   80.4%;  Pred. No. 5.4e-17;
  Matches  111;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy       2651 TGTGGGTTTTTTCAGGGGAGTTTGTGTGGAAGAGTCACAAATGGGACCGGGAGTTAATCT 2710
              ||  | ||||   ||||||||||||||||||| ||||    |||| |||| |||| ||||
Db         83 TGCTGTTTTTAAAAGGGGAGTTTGTGTGGAAGGGTCATGCCTGGGCCCGGCAGTTGATCT 142

Qy       2711 CAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAAGGTCACAACA 2770
              ||||||| |||||| ||  |||||| || |||||||||||||||||  | | ||  ||||
Db        143 CAGAGAGGTGGAAGGATGCCCCCAGTCCCGTGGATGCTGCATTCCGCTATGATCGTAACA 202

Qy       2771 GTGTCTTTCTGATCAAGG 2788
              ||||| ||||||||||||
Db        203 GTGTCCTTCTGATCAAGG 220


RESULT 13
US-09-960-352-2026
; Sequence 2026, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 2026
;   LENGTH: 373
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 09-LIB34-031-Q1-E1-C1
US-09-960-352-2026

  Query Match             3.2%;  Score 94.8;  DB 9;  Length 373;
  Best Local Similarity   80.4%;  Pred. No. 7.4e-17;
  Matches  111;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy       2651 TGTGGGTTTTTTCAGGGGAGTTTGTGTGGAAGAGTCACAAATGGGACCGGGAGTTAATCT 2710
              ||  | ||||   ||||||||||||||||||| ||||    |||| |||| |||| ||||
Db        106 TGCTGTTTTTAAAAGGGGAGTTTGTGTGGAAGGGTCATGCCTGGGCCCGGCAGTTGATCT 165

Qy       2711 CAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAAGGTCACAACA 2770
              ||||||| |||||| ||  |||||| || |||||||||||||||||  | | ||  ||||
Db        166 CAGAGAGGTGGAAGGATGCCCCCAGTCCCGTGGATGCTGCATTCCGCTATGATCGTAACA 225

Qy       2771 GTGTCTTTCTGATCAAGG 2788
              ||||| ||||||||||||
Db        226 GTGTCCTTCTGATCAAGG 243


RESULT 14
US-09-960-352-9132
; Sequence 9132, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9132
;   LENGTH: 384
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 39-LIB34-014-Q1-E1-B4
US-09-960-352-9132

  Query Match             3.2%;  Score 94.8;  DB 9;  Length 384;
  Best Local Similarity   80.4%;  Pred. No. 7.6e-17;
  Matches  111;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy       2651 TGTGGGTTTTTTCAGGGGAGTTTGTGTGGAAGAGTCACAAATGGGACCGGGAGTTAATCT 2710
              ||  | ||||   ||||||||||||||||||| ||||    |||| |||| |||| ||||
Db        218 TGCTGTTTTTAAAAGGGGAGTTTGTGTGGAAGGGTCATGCCTGGGCCCGGCAGTTGATCT 277

Qy       2711 CAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAAGGTCACAACA 2770
              ||||||| |||||| ||  |||||| || |||||||||||||||||  | | ||  ||||
Db        278 CAGAGAGGTGGAAGGATGCCCCCAGTCCCGTGGATGCTGCATTCCGCTATGATCGTAACA 337

Qy       2771 GTGTCTTTCTGATCAAGG 2788
              ||||| ||||||||||||
Db        338 GTGTCCTTCTGATCAAGG 355


RESULT 15
US-09-960-352-4209
; Sequence 4209, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4209
;   LENGTH: 396
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 18-LIB34-042-Q1-E1-E9
US-09-960-352-4209

  Query Match             3.2%;  Score 94.8;  DB 9;  Length 396;
  Best Local Similarity   80.4%;  Pred. No. 7.7e-17;
  Matches  111;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy       2651 TGTGGGTTTTTTCAGGGGAGTTTGTGTGGAAGAGTCACAAATGGACCGGGAGTTAATCT 2710
              ||  | ||||    |||||||||||||||||| ||||    |||| |||| |||| ||||
Db        224 TGCTGTTTTTAAAAGGGGAGTTTGTGTGGAAGGGTCATGCCTGGGCCCGGCAGTTGATCT 283

Qy       2711 CAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAAGGTCACAACA 2770
              ||||||| |||||| ||  |||||| || |||||||||||||||||  | | ||  ||||
Db        284 CAGAGAGGTGGAAGGATGCCCCCAGTCCCGTGGATGCTGCATTCCGCTATGATCGTAACA 343

Qy       2771 GTGTCTTTCTGATCAAGG 2788
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Db        344 GTGTCCTTCTGATCAAGG 361

Search completed: June  8, 2004, 23:18:02
Job time : 830.5 secs
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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2004  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         June  8, 2004, 17:11:50 ; Search time 142 Seconds
                                           (without alignments)
                                          11724.315 Million cell updates/sec

Title:          US-09-900-448-3_COPY_1_3000
Perfect score:  3000
Sequence:       1 tccctctccccaggcaggcc..........tggctgttcttcagtcctag 3000

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters:      1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Issued_Patents_NA:*
                1:  /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                2:  /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                3:  /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                4:  /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                5:  /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                6:  /cgn2_6/ptodata/2/ina/backfiles1.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                     SUMMARIES
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Result              Query
  No.     Score     Match Length DB  ID                        Description
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    2      49.2      1.6    7218  1  US-08-232-463-14          Sequence 14, Appl
 c  3      43.6      1.5   92139  4  US-09-918-686-1           Sequence 1, Appli
    4      42.8      1.4    5852  1  US-07-867-106-2           Sequence 2, Appli
 c  5      42.6      1.4   38653  4  US-09-922-445-1           Sequence 1, Appli
    6        42      1.4   87350  3  US-08-781-891-79          Sequence 79, Appl
    7        42      1.4   87350  4  US-09-618-166-79          Sequence 79, Appl
    8        42      1.4   87543  4  US-09-791-211-3           Sequence 3, Appli
 c  9      41.2      1.4     505  4  US-09-621-976-15639       Sequence 15639, A
   10        41      1.4     815  4  US-09-833-381-691         Sequence 691, App
   11        41      1.4   43795  3  US-08-742-185-101         Sequence 101, App
 c 12        41      1.4  118067  4  US-09-497-855A-32         Sequence 32, Appl
 c 13      40.8      1.4     569  4  US-09-461-325-44          Sequence 44, Appl
 c 14      40.8      1.4     569  4  US-10-012-542-44          Sequence 44, Appl
 c 15      40.8      1.4    1126  4  US-09-389-956-7           Sequence 7, Appli
 c 16      40.8      1.4    1210  4  US-09-443-041A-29         Sequence 29, Appl
   17      40.6      1.4     270  2  US-08-520-678A-30         Sequence 30, Appl
   18      40.6      1.4     270  3  US-08-897-126-30          Sequence 30, Appl
 c 19      40.6      1.4     969  4  US-09-023-655-66          Sequence 66, Appl
   20      40.4      1.3     832  4  US-09-621-976-2813        Sequence 2813, Ap
   21      40.2      1.3     196  4  US-09-644-460-40          Sequence 40, Appl
 c 22      40.2      1.3     240  4  US-09-621-976-1324        Sequence 1324, Ap
 c 23      40.2      1.3     249  4  US-09-621-976-1322        Sequence 1322, Ap
   24      40.2      1.3     260  2  US-08-520-678A-29         Sequence 29, Appl
   25      40.2      1.3     260  3  US-08-897-126-29          Sequence 29, Appl
 c 26      40.2      1.3     675  4  US-09-621-976-2461        Sequence 2461, Ap
 c 27      40.2      1.3    1560  4  US-09-227-357-34          Sequence 34, Appl
 c 28      40.2      1.3    2407  3  US-09-370-807-7           Sequence 7, Appli
 c 29      40.2      1.3    2407  4  US-09-921-259-7           Sequence 7, Appli
   30      40.2      1.3   13146  2  US-08-724-354D-3          Sequence 3, Appli
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 c 32        40      1.3    1198  3  US-09-248-335-27          Sequence 27, Appl
   33        40      1.3   63588  4  US-09-873-404-3           Sequence 3, Appli
 c 34      39.8      1.3    1008  4  US-09-780-641-1           Sequence 1, Appli
 c 35      39.8      1.3    1921  2  US-08-557-128-11          Sequence 11, Appl
 c 36      39.8      1.3    1925  4  US-09-148-545-128         Sequence 128, App
 c 37      39.8      1.3    6755  3  US-08-931-999-4           Sequence 4, Appli
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   39      39.8      1.3   15328  4  US-09-362-230-33          Sequence 33, Appl
   40      39.8      1.3   15328  5  PCT-US94-07926-33         Sequence 33, Appl
 c 41      39.6      1.3    2065  2  US-08-968-751-1           Sequence 1, Appli
 c 42      39.4      1.3     832  4  US-09-621-976-2813        Sequence 2813, Ap
 c 43      39.4      1.3    1813  3  US-09-071-224-3           Sequence 3, Appli
 c 44      39.4      1.3    2852  3  US-09-027-137-2           Sequence 2, Appli
 c 45      39.4      1.3    2852  4  US-09-344-441-2           Sequence 2, Appli

                                    ALIGNMENTS

RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match              2.0%;  Score 60.8;  DB 1;  Length 7218;
  Best Local Similarity   8.0%;  Pred. No. 4e-07;
  Matches   35;  Conservative  224;  Mismatches  181;  Indels    0;  Gaps    0;

Qy         25 AAAATCTGTAGGATTCAGACAGGGTTCTGACAGCTGAAGACAAGTTGTTGAGGAAATTCC 84
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Qy         85 TGATGGAGGATCATGGGGTGCTCAGGAGGGAGAATATAAGGTTTCAGAGGCTGAGAGGGA 144
               ||    ||  |: :::: :   ::::::::::: : ::::    :::::  ::::::::
Db       1446 AGAATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1387

Qy        145 AAGAAAAGGTGAGGGGGAGTCTTAGAATAGTGGCTCCCATTGCCCAACACCCAGAAAGAA 204
              ::::::::: :::::::::    :::: :: ::     :  :   :: :   ::::::::
Db       1386 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1327

Qy        205 GACATGCCCTGCAATGGGGAGAAGGTGAGTATGAGACATTGGCTGTAGCAGCGATGGCAT 264
              :: : :    : :: :::::::::: ::: : :::: :  ::  : :: :: :: :: :
Db       1326 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1267

Qy        265 TGCCCAGGCTGCCAAGGACTCAGAGAGTCCAGCCTTGCCCACTGACCTATGAGGAGGGAA 324
               :   :::  :  :::::   ::::::   ::    :   :  ::   : ::::::::::
Db       1266 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1207

Qy        325 TGATGTTCACAGCACATTTTCATTCGTAAGTCAGGAGAGGACATTGAGCCTGATGGCAGA 384
               :: :   : :: : :     :   : :::  ::::::::: :  :::   :: :: :::
Db       1206 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1147

Qy        385 GGCCTGGTGACATGTTGTTCCAGAGGTTCCGGAATGTGTGTTTTCCTGTTGGAAGGAAAC 444
              ::   :: :: : :  :    :::::    :::: : : :       :  :::::::::
Db       1146 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1087

Qy        445 TTCGCAGAGTAGAAAAGGGA 464
                 : :::: ::::::::::
Db       1086 RRRRRRRRRRRRRRRRRRRR 1067


RESULT 2
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
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;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             1.6%;  Score 49.2;  DB 1;  Length 7218;
  Best Local Similarity   5.7%;  Pred. No. 0.0012;
  Matches   24;  Conservative  218;  Mismatches  176;  Indels    0;  Gaps    0;

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              ::::  ::::::   ::: :::: ::: :::  :: : ::::: : :::: :: ::::::
Db       1071 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1130

Qy       2359 GGTTTTTTTTTTTTTTTTTTTTTTTTACTTTGCCATCTCCCTACCTCCACCCCAGAACGC 2418
                :::::::::::::::::::::::: :::: :: ::::::: ::::: ::::    : :
Db       1131 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1190

Qy       2419 TGCTCAGATGGCTGGAGCTTTGATGCTACCACCCTGGATGACAATGGAACCATGCTGTTT 2478
              : :::   :  ::    ::::  : :: :: ::::   :  :  :    :: : :: :::
Db       1191 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1250

Qy       2479 TTTAAAGGTAGGAGGGACTGAGGTTAGGGCGTTTAGGACCTTAGACTTACTCTCCTTCAC 2538
              :::     :        ::    ::    : :::    ::::   ::: ::::::::: :
Db       1251 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1310

Qy       2539 AAAGGGTGTCCCTGTCTGTGGGAGGTCTTAGGAATTATCTGATGGTATCACTGACAGCTT 2598
                    : ::::: ::: :      ::::     ::  ::: :  :  :: ::  :  :::
Db       1311 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1370

Qy       2599 CTCTCAAGCTATCTCAGTAGGTCAAAGGTTTCTCACTGGGCCCCTCAGTGAGTGTGGGTT 2658
              :::::   ::  ::::  :   ::     :::::: ::   ::::::  :   : :   ::
Db       1371 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1430

Qy       2659 TTTTCAGGGGAGTTTGTGTGGAAGAGTCACAAATGGGACCGGGAGTTAATCTCAGAGA 2716
              ::::      | ||  | |       | ||  | | | |  |  || ||||  |||  ||
Db       1431 YYYYGTACCAAATTCTTCTATCTCTTTAACTACTTGCATAGATAGGTAATTACAGTGA 1488


RESULT 3
US-09-918-686-1/c
; Sequence 1, Application US/09918686
; Patent No. 6475739
; GENERAL INFORMATION:
;  APPLICANT: Brunkow, Mary
;  APPLICANT:  Proll, Sean
;  APPLICANT:  Paeper, Bryan
;  APPLICANT:  Staehling-Hampton, Karen
;  TITLE OF INVENTION: METHODS FOR IDENTIFYING
;  TITLE OF INVENTION:  GENOMIC DELETIONS
;  FILE REFERENCE: 240083.515
;  CURRENT APPLICATION NUMBER: US/09/918,686
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 92139
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 7043, 8369, 8401
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-686-1

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  Best Local Similarity   65.3%;  Pred. No. 0.38;
  Matches     64;  Conservative     0;  Mismatches    34;  Indels     0;  Gaps     0;

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               ||| ||||||||||||| | || || ||  ||| |||||||| || |||||||     ||
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Qy         969 GATATATAATGGTAAACAAGACAGGCAAAACAAAGCAA 1006
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RESULT 4
US-07-867-106-2
; Sequence 2, Application US/07867106
; Patent No. 5389526
;  GENERAL INFORMATION:
;    APPLICANT:  Slade, Martin B
;    APPLICANT:  Chang, Andy C M
;    APPLICANT:  Williams, Keith L
;    TITLE OF INVENTION:  Improved Plasmid Vectors for Cellular
;    TITLE OF INVENTION:  Slime Moulds of the Genus Dictyostelium
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
;      STREET:  One Liberty Place 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/867,106
;      FILING DATE:  19920625
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PJ 7187
;      APPLICATION NUMBER:  PCT/AU90/00530
;      FILING DATE:  02-NOV-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Feeney, Joanne Longo
;      REGISTRATION NUMBER:  35,134
;      REFERENCE/DOCKET NUMBER:  RICB-0002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5852 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2378..5038
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2378..5038
US-07-867-106-2

  Query Match             1.4%;  Score 42.8;  DB 1;  Length 5852;
  Best Local Similarity   50.0%;  Pred. No. 0.089;
  Matches  107;  Conservative     0;  Mismatches  107;  Indels     0;  Gaps     0;

Qy         888 AAATGCATTTTTGCATTTTTTTCATTCAACAAATATTTCTGGAACAACTCTTATATGCCA 947
               | ||  ||   |||| |  | | | | || |||    | |  || || | ||| |  |
Db        5275 ATATTAATCCGTGCAGTACTATTAATTAAAAAAATACTTTAAAAAAAATTTTAAAAACAT 5334

Qy         948 GGCACTATTTTAGGAGTCAGGGATATATAATGGTAAACAAGACAGGCAAAACAAAGCAAA 1007
               || |   | |   ||   |  |||   ||||  | || |  | |   |  | |     ||
Db        5335 GGAAAATTATATAGATCGATAGATCACTAATTTTTAAAATTAAATATATTAAATTTATAA 5394

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                 |   |    |||||  | |||   | |   ||  ||  |||| || |||||  ||  |
Db        5395 AAATTGAAGTTCATCAAGATATATAGATAATTATTTAATTATTTGAATTTTTAAAAAAAA 5454

Qy        1068 AAATAAAACAAGCAAGGGTCTGAAATGGCTAGAT 1101
               ||| |||| ||  ||     | ||||   |  ||
Db        5455 AAAAAAAAAAAAAAAAAAAATCAAATATGTTTAT 5488

RESULT 5
US-09-922-445-1/c
; Sequence 1, Application US/09922445
; Patent No. 6528268
; GENERAL INFORMATION:
;  APPLICANT: Andersson, Maria K.
;  APPLICANT:  Berglund, Lars G. T.
;  APPLICANT:  Reneland, Rikard  H.
;  APPLICANT:  Adam, Gail I. R.
;  TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
;  FILE REFERENCE: GG126US
;  CURRENT APPLICATION NUMBER: US/09/922,445
;  CURRENT FILING DATE:  2001-08-03
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 38653
;   TYPE: DNA
;   ORGANISM: homo sapiens
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: (1)..(26156)
;   OTHER INFORMATION:
;   NAME/KEY: misc_feature
;   LOCATION: (24801)..(24801)
;   OTHER INFORMATION: nucleotide 24801 is a single nucleotide polymorphism which can be
;   OTHER INFORMATION: A or G
;   NAME/KEY: misc_feature
;   LOCATION: (24941)..(24941)
;   OTHER INFORMATION: nucleotide 24941 is a single nucleotide polymorphism which can be
;   OTHER INFORMATION: T or C
;   NAME/KEY: exon
;   LOCATION: (26157)..(26252)
;   OTHER INFORMATION:
;   NAME/KEY: Intron
;   LOCATION: (26253)..(26401)
;   OTHER INFORMATION:
;   NAME/KEY: exon
;   LOCATION: (26402)..(26543)
;   OTHER INFORMATION:
;   NAME/KEY: Intron
;   LOCATION: (26544)..(27024)
;   OTHER INFORMATION:
;   NAME/KEY: exon
;   LOCATION: (27025)..(27178)
;   OTHER INFORMATION:
;   NAME/KEY: Intron
;   LOCATION: (27179)..(30519)
;   OTHER INFORMATION:
;   NAME/KEY: misc_feature
;   LOCATION: (27645)..(27645)
;   OTHER INFORMATION: nucleotide 27645 is a single nucleotide polymorphism which can be
;   OTHER INFORMATION: C or G
;   NAME/KEY: exon
;   LOCATION: (30520)..(30681)
;   OTHER INFORMATION:
;   NAME/KEY: Intron
;   LOCATION: (30682)..(30894)
;   OTHER INFORMATION:
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;   LOCATION: (30895)..(31027)
;   OTHER INFORMATION:
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;   LOCATION: (31028)..(31747)
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;   LOCATION: (31748)..(31841)
;   OTHER INFORMATION:
;   NAME/KEY: Intron
;   LOCATION: (31842)..(32400)
;   OTHER INFORMATION:
;   NAME/KEY: misc_feature
;   LOCATION: (32163)..(32163)
;   OTHER INFORMATION: nucleotide 32163 is a single nucleotide polymorphism which can be
;   OTHER INFORMATION: A or C
;   NAME/KEY: exon
;   LOCATION: (32401)..(32528)
;   OTHER INFORMATION:
;   NAME/KEY: Intron
;   LOCATION: (32529)..(33414)
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;   NAME/KEY: misc_feature
;   LOCATION: (32614)..(32614)
;   OTHER INFORMATION: nucleotide 32614 is a single nucleotide polymorphism which can be
;   OTHER INFORMATION: A or G
;   NAME/KEY: exon
;   LOCATION: (33415)..(33597)
;   OTHER INFORMATION:
;   NAME/KEY: Intron
;   LOCATION: (33598)..(34314)
;   OTHER INFORMATION:
;   NAME/KEY: exon
;   LOCATION: (34315)..(34588)
;   OTHER INFORMATION:
;   NAME/KEY: Intron
;   LOCATION: (34589)..(36404)
;   OTHER INFORMATION:
;   NAME/KEY: exon
;   LOCATION: (36405)..(36523)
;   OTHER INFORMATION:
;   NAME/KEY: Intron
;   LOCATION: (36524)..(38341)
;   OTHER INFORMATION:
;   NAME/KEY: exon
;   LOCATION: (38342)..(38653)
;   OTHER INFORMATION:
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: Genbank/AC004923
;   DATABASE ENTRY DATE: 1999-12-21
;   RELEVANT RESIDUES: (1)..(38653)
US-09-922-445-1

  Query Match              1.4%;  Score 42.6;  DB 4;  Length 38653;
  Best Local Similarity   67.4%;  Pred. No. 0.4;
  Matches   60;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          904 TTTTTTCATTCAACAAATATTTCTGGAACAACTCTTATATGCCAGGCACTATTTTAGGAG 963
                | | ||||| || ||| |||||   || || ||  ||| ||||||| ||| || ||||
Db        14573 TGTATTCATGCAGCAACTATTTGCTGAGCACCTACTATGTGCCAGGTACTGTTCTAGGCT 14514

Qy          964 TCAGGGATATATAATGGTAAACAAGACAG 992
                   ||||||||  |  | | | || ||||
Db        14513 CTGGGGATATAGCAGAGAATAAAACACAG 14485


RESULT 6
US-08-781-891-79
; Sequence 79, Application US/08781891
; Patent No. 6090620
;  GENERAL INFORMATION:
;    APPLICANT:  Fu, Ying-Hui
;    APPLICANT:  Yu, Chang-En
;    APPLICANT:  Oshima, Junko
;    APPLICANT:  Mulligan, John T.
;    APPLICANT:  Schellenberg, Gerald D.
;    TITLE OF INVENTION:  GENE AND GENE PRODUCTS RELATED TO
;    TITLE OF INVENTION:  WERNER'S SYNDROME
;    NUMBER OF SEQUENCES:  209
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/781,891
;      FILING DATE:  27-DEC-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6090620tenburg Ph.D., Carol
;      REGISTRATION NUMBER:  39,317
;      REFERENCE/DOCKET NUMBER:  240052.419
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  79:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  87350 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-781-891-79

  Query Match              1.4%;  Score 42;  DB 3;  Length 87350;
  Best Local Similarity   66.7%;  Pred. No. 1.1;
  Matches   60;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          911 ATTCAACAAATATTTCTGGAACAACTCTTATATGCCAGGCACTATTTTAGGAGTCAGGGA 970
                ||||||||||||||| | || ||  |  ||| ||||||||||| || | | ||     |
Db        64933 ATTCAACAAATATTTATTGAGCACTTACTATGTGCCAGGCACTGTTGTTGTAGGTGCTGG 64992

Qy          971 TATATAATGGTAAACAAGACAGGCAAAACA 1000
                 ||| |    | ||||| | | |  |||||
Db        64993 AATACAGCAATGAACAAAAAAAGTGAAACA 65022


RESULT 7
US-09-618-166-79
; Sequence 79, Application US/09618166
; Patent No. 6583112
;  GENERAL INFORMATION:
;       APPLICANT: Fu, Ying-Hui
;                  Yu, Chang-En
;                  Oshima, Junko
;                  Mulligan, John T.
;                  Schellenberg, Gerald D.
;       TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
;                           WERNER'S SYNDROME
;       NUMBER OF SEQUENCES: 209
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Seed Intellectual Property Law Group
;            STREET: 701 Fifth Avenue, Suite 6300
;            CITY: Seattle
;            STATE: Washington
;            COUNTRY: USA
;            ZIP: 98104-7092
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/618,166
;             FILING DATE: 17-Jul-2000
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McMasters, David D.
;             REGISTRATION NUMBER: 33,963
;             REFERENCE/DOCKET NUMBER: 240052.419C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 622-4900
;             TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 79:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 87350 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-618-166-79

  Query Match             1.4%;  Score 42;  DB 4;  Length 87350;
  Best Local Similarity   66.7%;  Pred. No. 1.1;
  Matches   60;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy        911 ATTCAACAAATATTTCTGGAACAACTCTTATATGCCAGGCACTATTTTAGGAGTCAGGGA 970
              ||||||||||||||| | || ||  |  ||| ||||||||||| || | | ||     |
Db      64933 ATTCAACAAATATTTATTGAGCACTTACTATGTGCCAGGCACTGTTGTTGTAGGTGCTGG 64992

Qy        971 TATATAATGGTAAACAAGACAGGCAAAACA 1000
               ||| |    | ||||| | | |  |||||
Db      64993 AATACAGCAATGAACAAAAAAAGTGAAACA 65022


RESULT 8
US-09-791-211-3
; Sequence 3, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
;  APPLICANT:  Donna T. Ward
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION:  ANTISENSE MODULATION OF WRN EXPRESSION
;  FILE REFERENCE:  RTS-0205
;  CURRENT APPLICATION NUMBER: US/09/791,211
;  CURRENT FILING DATE:  2001-02-23
;  NUMBER OF SEQ ID NOS:  90
; SEQ ID NO 3
;   LENGTH: 87543
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 7421
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 7427
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 11609
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 12605
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 12742
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29370
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29422
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29979
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29980
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 29981
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 30136
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 30140
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 31205
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 31206
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 31592
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 33095
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 33160
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 34066
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 34072
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 36816
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 39020
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 42164
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 42459
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 46808
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 46823
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 46826
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 47291
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 52786
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 52787
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 53384
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 54684
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 59215
;   OTHER INFORMATION: unknown
;    NAME/KEY: unsure
;    LOCATION: 59235
;    OTHER INFORMATION: unknown
;    NAME/KEY: unsure
;    LOCATION: 59242
;    OTHER INFORMATION: unknown
;    NAME/KEY: unsure
;    LOCATION: 63290
;    OTHER INFORMATION: unknown
;    NAME/KEY: unsure
;    LOCATION: 66614
;    OTHER INFORMATION: unknown
;    NAME/KEY: unsure
;    LOCATION: 68660
;    OTHER INFORMATION: unknown
;    NAME/KEY: unsure
;    LOCATION: 68697
;    OTHER INFORMATION: unknown
;    NAME/KEY: unsure
;    LOCATION: 68718
;    OTHER INFORMATION: unknown
;    NAME/KEY: unsure
;    LOCATION: 68733
;    OTHER INFORMATION: unknown
;    NAME/KEY: unsure
;    LOCATION: 68739
;    OTHER INFORMATION: unknown
;    NAME/KEY: unsure
;    LOCATION: 69785
;    OTHER INFORMATION: unknown
;    NAME/KEY: unsure
;    LOCATION: 79134
;    OTHER INFORMATION: unknown
;    NAME/KEY: unsure
;    LOCATION: 79198
;    OTHER INFORMATION: unknown
;    NAME/KEY: unsure
;    LOCATION: 86336
;    OTHER INFORMATION: unknown
;    OTHER INFORMATION:
US-09-791-211-3

  Query Match             1.4%;  Score 42;  DB 4;  Length 87543;
  Best Local Similarity   66.7%;  Pred. No. 1.1;
  Matches   60;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          911 ATTCAACAAATATTTCTGGAACAACTCTTATATGCCAGGCACTATTTTAGGAGTCAGGGA 970
                ||||||||||||||| | || ||  |  ||| |||||||||||| || | | ||     |
Db        65126 ATTCAACAAATATTTATTGAGCACTTACTATGTGCCAGGCACTGTTGTTGTAGGTGCTGG 65185

Qy          971 TATATAATGGTAAACAAGACAGGCAAAACA 1000
                 ||| |    | ||||| | | |  |||||
Db        65186 AATACAGCAATGAACAAAAAAAGTGAAACA 65215

RESULT 9
US-09-621-976-15639/c
; Sequence 15639, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 15639
;   LENGTH: 505
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-15639

  Query Match             1.4%;  Score 41.2;  DB 4;  Length 505;
  Best Local Similarity   15.4%;  Pred. No. 0.046;
  Matches   49;  Conservative  146;  Mismatches  119;  Indels    4;  Gaps    2;

Qy          351 TAAGTCAGGAGAGGACATTGAGCCTGATGGCAGAGGCCTGGTGACATGTTGTTCCAGAGG 410
                ::::  | | :  |:  :|: : :||::|:: ::::::| : |: :|::: |:   :  |
Db          367 KMRRMAAAGGSYCGMTSYTSGSKMTGRKGSMTKRKRMMTYS-GMWWTSYKCTKTGKKYTG 309

Qy          411 TTCCGGAATGTGTGTTTTCCTGTTGGAAGGAAACTTCGCAGAGTAGAAAAGGGATCTGAG 470
                ::: : ::| |::::: ::: | : : ::::|::::: :| :  ::| | : :: ::||:
Db          308 WKSKKTRWTCTSWRKYMWMMSGCWARSMKSWARSWYSMMACWCMMSASAYRARRSMYGAR 249

Qy          471 ACTTTTGGTAAGATTATATATGGGACTGTCAGGGGTCTGGAGCCATCTGTGAGGGATCAG 530
                ::    |  :::|   :  | |:: : :  ::: : : |:|::|:      :: :  |:|
Db          248 RSMMRAGAGWWRARRGKKRARGKSSMMRSKMSSMRMSAGKARMCRRWMWSCRRMSYSCMG 189

Qy          531 GGCCCTTTCAGCCTTGGCTAGGGAGCAGGGGTCCTGGAACTTCATCCTGGCCCATAGCTG 590
                ::|::   |:| | :   :|:   ::|:: |::: | ::|:     ::| : :: ::  :
Db          188 SKCMS---CRGTCAKMWRYARYAKRYASSMGKYMMGCRWCYAKCARMYGYYRSRSRSTGS 132

Qy          591 AGTCTGCCCATAATTCTTTTCTGACTCACTAGGCAAATCTCACACAGAAATGGGGCAGCT 650
                :|  ::   :: ::::: :  :     |   | :|:|:  :|:::|  :  :  ::::
Db          131 RGMKYRRRKMYYMWKYWMWSWWCYRMGAAMYGMSARAYRMYASMSACKMCSRMMKMMSWS 72

Qy          651 TTGGGAGTGGGCCCAGGA 668
                 : : :: : :| : |::
Db           71 MWMRCWRSRYRCWMSGKW 54

RESULT 10
US-09-833-381-691
; Sequence 691, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
;  FILE REFERENCE: 5800-119
;  CURRENT APPLICATION NUMBER: US/09/833,381
;  CURRENT FILING DATE:  2001-04-11
;  PRIOR APPLICATION NUMBER: 09/516,448
;  PRIOR FILING DATE: 2000-02-29
;  NUMBER OF SEQ ID NOS: 2050
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 691
;   LENGTH: 815
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(815)
;   OTHER INFORMATION: n = A,T,C or G
US-09-833-381-691

  Query Match             1.4%;  Score 41;  DB 4;  Length 815;
  Best Local Similarity   66.3%;  Pred. No. 0.074;
  Matches   59;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy         2301 CTGACTCCCTAAGTCTGTCTTATCTGTCTGGTTGTGTCTCTGCATTTTATCACCTTCTGG 2360
                ||  ||| |||||  |  |||  | |  || || | | | |   |||| |    || |
Db           40 CTACCTCACTAAGGATAGCTTGCCCGAATGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 99

Qy         2361 TTTTTTTTTTTTTTTTTTTTTTTTACTTT 2389
                ||||||||||||||||||||||||  |||
Db          100 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 128

RESULT 11
US-08-742-185-101
; Sequence 101, Application US/08742185
; Patent No. 6020476
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  Page, David C.
;    APPLICANT:  Reijo, Renee
;    APPLICANT:  Saxena, Richa
;    APPLICANT:  Hawkins,Trevor
;    APPLICANT:  Reeve, Mary Pat
;    TITLE OF INVENTION:  DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
;    NUMBER OF SEQUENCES:  102
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/742,185
;      FILING DATE:  30-OCT-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/690,734
;      FILING DATE:  31-JUL-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/310,429
;      FILING DATE:  22-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  WHI94-07A2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  101:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  43795 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-742-185-101

  Query Match             1.4%;  Score 41;  DB 3;  Length 43795;
  Best Local Similarity   63.9%;  Pred. No. 1.3;
  Matches   62;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy       2293 GTGAGGCCCTGACTCCCTAAGTCTGTCTTATCTGTCTGGTTGTGTCTCTGCATTTTATCA 2352
              | |||||  |   |  |  | ||  |||| |   ||    |  |||| | ||  || ||
Db      16660 GGGAGGCTGTTTATTACAGATTCAATCTTCTTACTCATAATTGGTCTGTTCAGGTTTTCT 16719

Qy       2353 CCTTCTGGTTTTTTTTTTTTTTTTTTTTTTTTTACTTT 2389
                ||||  ||||||||||||||||||||||||  |||
Db      16720 ATTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 16756

RESULT 12
US-09-497-855A-32/c
; Sequence 32, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
;  APPLICANT: Huang, Tim
;  TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
;  FILE REFERENCE: UMO1523
;  CURRENT APPLICATION NUMBER: US/09/497,855A
;  CURRENT FILING DATE:  2000-02-04
;  PRIOR APPLICATION NUMBER: 60/120,592
;  PRIOR FILING DATE: 1999-02-18
;  PRIOR APPLICATION NUMBER: 60/118,760
;  PRIOR FILING DATE: 1999-02-05
;  NUMBER OF SEQ ID NOS: 54
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;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
;   LENGTH: 118067
;   TYPE: DNA
;   ORGANISM: Homo sapiens;
US-09-497-855A-32

  Query Match             1.4%;  Score 41;  DB 4;  Length 118067;
  Best Local Similarity   69.1%;  Pred. No. 2.7;
  Matches   56;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy        893 CATTTTTGCATTTTTTTCATTCAACAAATATTTCTGGAACAACTCTTATATGCCAGGCAC 952
              ||||||     |    ||||||||| ||| ||| | || || ||  ||| |||||||||
Db      35145 CATTTTACAGATGGACTCATTCAACTAATGTTTATTGAGCATCTTCTATGTGCCAGGCAA 35086

Qy        953 TATTTTAGGAGTCAGGGATAT 973
              |||| ||   | ||| |||||
Db      35085 TATTCTAAATGCCAGTGATAT 35065

RESULT 13
US-09-461-325-44/c
; Sequence 44, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029P1
;  CURRENT APPLICATION NUMBER: US/09/461,325A
;  CURRENT FILING DATE: 1999-12-14
;  EARLIER APPLICATION NUMBER: PCT/US99/13418
;  EARLIER FILING DATE: 1999-06-15
;  EARLIER APPLICATION NUMBER: 60/089,507
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/089,508
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/089,509
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/089,510
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/090,112
;  EARLIER FILING DATE: 1998-06-22
;  EARLIER APPLICATION NUMBER: 60/090,113
;  EARLIER FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-461-325-44

  Query Match             1.4%;  Score 40.8;  DB 4;  Length 569;
  Best Local Similarity   58.1%;  Pred. No. 0.066;
  Matches   72;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy       2314 TCTGTCTTATCTGTCTGGTTGTGTCTCTGCATTTTATCACCTTCTGGTTTTTTTTTTTTT 2373
              | | | || | | | |  || | | | |   |||| |    || |  |||||||||||||
Db        504 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 445

Qy       2374 TTTTTTTTTTTACTTTGCCATCTCCCTACCTCCACCCCAGAACGCTGCTCAGATGGCTGG 2433
              |||||||||||     |   | | || |   || |  || ||||   ||    |||  ||
Db        444 TTTTTTTTTTTGGAGGGGGTTTGCCAAATCCCGCTGCAAAACGGACTGCCCTGGAGGG 385

Qy       2434 AGCT 2437
               |||
Db        384 TGCT 381

RESULT 14
US-10-012-542-44/c
; Sequence 44, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029P1
;  CURRENT APPLICATION NUMBER: US/10/012,542
;  CURRENT FILING DATE:  2001-12-12
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-012-542-44

  Query Match             1.4%;  Score 40.8;  DB 4;  Length 569;
  Best Local Similarity   58.1%;  Pred. No. 0.066;
  Matches   72;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

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; Sequence 7, Application US/09389956
; Patent No. 6586579
; GENERAL INFORMATION:
;  APPLICANT: Huang, Shi
;  TITLE OF INVENTION: PR-Domain Containing Nucleic Acids, Polypeptides,
;  TITLE OF INVENTION: Antibodies and Methods
;  FILE REFERENCE: P-LJ 3611
;  CURRENT APPLICATION NUMBER: US/09/389,956
;  CURRENT FILING DATE: 1999-09-03
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 1126
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (54)..(386)
US-09-389-956-7

  Query Match             1.4%;  Score 40.8;  DB 4;  Length 1126;
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Search completed: June  8, 2004, 19:11:57
Job time : 145 secs
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                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:          June  8, 2004, 18:54:10 ; Search time 829.5 Seconds
                                             (without alignments)
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Perfect score:   3000
Sequence:        1 tcttagttctacaccgctct..........ctccattgtcatcactgtgt 3000

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters:      5991872

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

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    3    445.2       14.8    495  10  US-09-918-995-32463           Sequence 32463, A
    4    441.6       14.7    480  10  US-09-918-995-31405           Sequence 31405, A
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; Sequence 3, Application US/09900448
; Publication No. US20030220488A1
; GENERAL INFORMATION:
;  APPLICANT: CECCARDI, Toni et al.
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001272
;  CURRENT APPLICATION NUMBER: US/09/900,448
;  CURRENT FILING DATE:  2001-07-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 13737
;   TYPE: DNA
;   ORGANISM: Human
US-09-900-448-3

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Db       5521 GCCCTAGCACTTGAGACCTGTCAGAATTCATCCACTTTCCCTGAGCTTGTGGATCTCACG 5580

Qy       2581 TGTCCTAGCTCTCACTTTAACTCCGTGTTGCGACACCTTGGCCCTTAATCTAGCCCCATT 2640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5581 TGTCCTAGCTCTCACTTTAACTCCGTGTTGCGACACCTTGGCCCTTAATCTAGCCCCATT 5640

Qy       2641 TCCATTCTGGATTTTCCCATTGCCCTCATATGGGAAACCCACACCCCACTAACCCCAGC 2700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5641 TCCATTCTGGATTTTCCCATTGCCCTCATATGGGAAACCCACACCCCACTAACCCCAGC 5700

Qy       2701 CATCTCTTCCACCTTGGACCTCACTCTGACCTCTGGCCTCCTTCTGTGTTCTCCTCACCC 2760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5701 CATCTCTTCCACCTTGGACCTCACTCTGACCTCTGGCCTCCTTCTGTGTTCTCCTCACCC 5760

Qy       2761 ATTTCTCTCTCCAGGCCATGGACACAGGAATGGGACTGGCCATGGGAACAGTACCCACCA 2820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5761 ATTTCTCTCTCCAGGCCATGGACACAGGAATGGGACTGGCCATGGGAACAGTACCCACCA 5820

Qy       2821 TGGCCCTGAGTATATGCGCTGTAGCCCACATCTAGTCTTGTCTGCACTGACGTCTGACAA 2880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5821 TGGCCCTGAGTATATGCGCTGTAGCCCACATCTAGTCTTGTCTGCACTGACGTCTGACAA 5880

Qy       2881 CCATGGTGCCACCTATGCCTTCAGTGGTGAGAGATGCCCCCAACTCCCCCAATGTGCTCT 2940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 CCATGGTGCCACCTATGCCTTCAGTGGTGAGAGATGCCCCCAACTCCCCCAATGTGCTCT 5940

Qy       2941 CACATCTCTTTTACTTGTATCTCCCATCCTTGACACATTTCTCCATTGTCATCACTGTGT 3000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5941 CACATCTCTTTTACTTGTATCTCCCATCCTTGACACATTTCTCCATTGTCATCACTGTGT 6000


RESULT 2
US-09-918-995-31396
; Sequence 31396, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31396
;   LENGTH: 533
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(533)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31396

  Query Match             15.3%;  Score 457.6;  DB 10;  Length 533;
  Best Local Similarity   98.9%;  Pred. No. 1.4e-131;
  Matches  460;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1479 GAGAAAGGATACCCAAAGTTGCTCCAAGATGAATTTCCTGGAATCCCATCCCCACTGGAT 1538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GAGAAAGGATACCCAAAGTTGCTCCAAGATGAATTTCCTGGAATCCCATCCCCACTGGAT 127

Qy       1539 GCAGCTGTGGAATGTCACCGTGGAGAATGTCAAGCTGAAGGCGTCCTCTTCTTCCAAGGT 1598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 GCAGCTGTGGAATGTCACCGTGGAGAATGTCAAGCTGAAGGCGTCCTCTTCTTCCAAGGT 187

Qy       1599 CAGTCCAGGCTGGAATCCAAGAACCTGGAGTAGTGGTGGGTTGGTAGTGATGCCAGTAGT 1658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CAGTCCAGGCTGGAATCCAAGAACCTGGAGTAGTGGTGGGTTGGTAGTGATGCCAGTAGT 247

Qy       1659 GATGGTGATAGTGGTAGTGATGGTGGTGGTGGAGCCACTATGTGGCTTTTTAAGGAAGGG 1718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GATGGTGATAGTGGTAGTGATGGTGGTGGTGGAGCCACTATGTGGCTTTTTAAGGAAGGG 307

Qy       1719 AAATAGAGAAGCCACGTATGGTCTAGAGGTCACGTGAGGGAAGGAGAGGAAGTCATTCTG 1778
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        308 AAATAGAGAAGCCACGTATGGTCTAAAGGTCACGTGAGGGAAGGAGAGGAAGTCATTCTG 367

Qy       1779 GTGAAGGCAACTGTGTGTAATTCTGTGTGAATAGTCCCTCATTGTTCCCCATGACCCTTA 1838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 GTGAAGGCAACTGTGTGTAATTCTGTGTGAATAGTCCCTCATTGTTCCCCATGACCCTTA 427

Qy       1839 GGACAAATCTACCCTCTTTAGTCTTACATACAAGTCTCTCCATGGCCAAATCCCTATTGG 1898
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 NGACAAATCTACCCTCTTTAGTCTTACATACAAGTCTCTCCATGGCCAAATCCCTATTGG 487

Qy       1899 CCCTTCAGCTTTGACTTTTATTATACTTTTACCTTAACACTAAGC 1943
              |||||||   |||||||||||||||||||||||||||||||||||
Db        488 CCCTTCAAGCTTGACTTTTATTATACTTTTACCTTAACACTAAGC 532


RESULT 3
US-09-918-995-32463
; Sequence 32463, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32463
;   LENGTH: 495
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(495)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32463

  Query Match             14.8%;  Score 445.2;  DB 10;  Length 495;
  Best Local Similarity   99.3%;  Pred. No. 9.8e-128;
  Matches  447;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1908 TTTGACTTTTATTATACTTTTACCTTAACACTAAGCTCCAGAAACCCTATGCTATTCTCT 1967
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         46 TCTGACTTTTATTATACTTTTACCTTAACACTAAGCTCCAGAAACCCTATGCTATTCTCT 105

Qy       1968 GTACACTCAGTTTGCTCCATGCTTTGGAATCTTTCCTCTCTCTGGGGTTCCATCTCTCCT 2027
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GTACACTCAGTTTGCTCCATGCTTTGGAATCTTTCCTCTCTCTGGGGTTCCATCTCTCCT 165

Qy       2028 TGTGTGCCTTTTAATTCCTACTTCAGATTTCACTTTAAGTATCATCTTCCCTGGGAAGTT 2087
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 TGTGTGCCTTTTAATTCCTACTTCAGATTTCACTTTAAGTATCATCTTCCCTGGGAAGTT 225

Qy       2088 TTCCCAGACTCTCCCCACTGCCTTTGCTGAGCTGATCCTGTGTGTTTTGCTGCTGAATTT 2147
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                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          226 TTCCCAGACTCTCCCCACTGCCTTTGCTGAGCTGATCCTGTGTGTTTTGCTGCTGAATTT 285

Qy         2148 TGGTGTATGATCACCCTCCTTTAGCCATCTCTCTGATGGCTGTGAGCTCCATGTGGTCAG 2207
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          286 TGGTGTATGATCACCCTCCTTTAGCCATCTCTCTGATGGCTGTGAGCTCCATGTGGTCAG 345

Qy         2208 TACCATTATCTGGCCCATCCTGGGACCCAGAGAAAGCACAAAGGAGGGCGTAACCCGGTC 2267
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          346 TACCATTATCTGGCCCATCCTGGGACCCAGAGAAAGCACAAAGGAGGGCGTAACCCGGTC 405

Qy         2268 TCACCAAATGCCTGTTGATTGATTGGACAAAGGTGACCGCGAGTGGTTCTGGGACTTGGC 2327
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          406 TCACCAAATGCCTGTTGATTGATTGGACAAAGGTGACCGCGAGTGGTTCTGGGACTTGGC 465

Qy         2328 TACGGGAACCATGAAGGAGCGTTCCTGGCC 2357
                |||||||||||||||||||||||||  |||
Db          466 TACGGGAACCATGAAGGAGCGTTCCCTGCC 495


RESULT 4
US-09-918-995-31405
; Sequence 31405, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31405
;   LENGTH: 480
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(480)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31405

  Query Match             14.7%;  Score 441.6;  DB 10;  Length 480;
  Best Local Similarity   99.1%;  Pred. No. 1.3e-126;
  Matches  444;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         1908 TTTGACTTTTATTATACTTTTACCTTAACACTAAGCTCCAGAAACCCTATGCTATTCTCT 1967
                | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           32 TCTGACTTTTATTATACTTTTACCTTAACACTAAGCTCCAGAAACCCTATGCTATTCTCT 91

Qy         1968 GTACACTCAGTTTGCTCCATGCTTTGGAATCTTTCCTCTCTCTGGGGTTCCATCTCTCCT 2027
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           92 GTACACTCAGTTTGCTCCATGCTTTGGAATCTTTCCTCTCTCTGGGGTTCCATCTCTCCT 151

Qy         2028 TGTGTGCCTTTTAATTCCTACTTCAGATTTCACTTTAAGTATCATCTTCCCTGGGAAGTT 2087
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          152 TGTGTGCCTTTTAATTCCTACTTCAGATTTCACTTTAAGTATCATCTTCCCTGGGAAGTT 211

Qy         2088 TTCCCAGACTCTCCCCACTGCCTTTGCTGAGCTGATCCTGTGTGTTTTGCTGCTGAATTT 2147
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          212 TTCCCAGACTCTCCCCACTGCCTTTGCTGAGCTGATCCTGTGTGTTTTGCTGCTGAATTT 271

Qy         2148 TGGTGTATGATCACCCTCCTTTAGCCATCTCTCTGATGGCTGTGAGCTCCATGTGGTCAG 2207
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          272 TGGTGTATGATCACCCTCCTTTAGCCATCTCTCTGATGGCTGTGAGCTCCATGTGGTCAG 331

Qy         2208 TACCATTATCTGGCCCATCCTGGGACCCAGAGAAAGCACAAAGGAGGGCGTAACCCGGTC 2267
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          332 TACCATTATCTGGCCCATCCTGGGACCCAGAGAAAGCACAAAGGAGGGCGTAACCCGGTC 391
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Qy         2268 TCACCAAATGCCTGTTGATTGATTGGACAAAGGTGACCGCGAGTGGTTCTGGGACTTGGC 2327
                |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db          392 TCACCAAATGCCTGTTGATTGATTGGACCAAGGTGACCGCGAGTGGTTCTGGGACTTGGC 451

Qy         2328 TACGGGAACCATGAAGGAGCGTTCCTGG 2355
                ||||||||||||||| |||||||||| |
Db          452 TACGGGAACCATGAAAGAGCGTTCCTTG 479


RESULT 5
US-09-918-995-31407
; Sequence 31407, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31407
;   LENGTH: 494
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(494)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31407

  Query Match             14.7%;  Score 441.4;  DB 10;  Length 494;
  Best Local Similarity   99.8%;  Pred. No. 1.5e-126;
  Matches  442;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         1908 TTTGACTTTTATTATACTTTTACCTTAACACTAAGCTCCAGAAACCCTATGCTATTCTCT 1967
                | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           52 TCTGACTTTTATTATACTTTTACCTTAACACTAAGCTCCAGAAACCCTATGCTATTCTCT 111

Qy         1968 GTACACTCAGTTTGCTCCATGCTTTGGAATCTTTCCTCTCTCTGGGGTTCCATCTCTCCT 2027
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          112 GTACACTCAGTTTGCTCCATGCTTTGGAATCTTTCCTCTCTCTGGGGTTCCATCTCTCCT 171

Qy         2028 TGTGTGCCTTTTAATTCCTACTTCAGATTTCACTTTAAGTATCATCTTCCCTGGGAAGTT 2087
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          172 TGTGTGCCTTTTAATTCCTACTTCAGATTTCACTTTAAGTATCATCTTCCCTGGGAAGTT 231

Qy         2088 TTCCCAGACTCTCCCCACTGCCTTTGCTGAGCTGATCCTGTGTGTTTTGCTGCTGAATTT 2147
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          232 TTCCCAGACTCTCCCCACTGCCTTTGCTGAGCTGATCCTGTGTGTTTTGCTGCTGAATTT 291

Qy         2148 TGGTGTATGATCACCCTCCTTTAGCCATCTCTCTGATGGCTGTGAGCTCCATGTGGTCAG 2207
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          292 TGGTGTATGATCACCCTCCTTTAGCCATCTCTCTGATGGCTGTGAGCTCCATGTGGTCAG 351

Qy         2208 TACCATTATCTGGCCCATCCTGGGACCCAGAGAAAGCACAAAGGAGGGCGTAACCCGGTC 2267
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          352 TACCATTATCTGGCCCATCCTGGGACCCAGAGAAAGCACAAAGGAGGGCGTAACCCGGTC 411

Qy         2268 TCACCAAATGCCTGTTGATTGATTGGACAAAGGTGACCGCGAGTGGTTCTGGGACTTGGC 2327
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          412 TCACCAAATGCCTGTTGATTGATTGGACAAAGGTGACCGCGAGTGGTTCTGGGACTTGGC 471

Qy         2328 TACGGGAACCATGAAGGAGCGTT 2350
                |||||||||||||||||||||||
Db          472 TACGGGAACCATGAAGGAGCGTT 494


RESULT 6
US-09-918-995-31269
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; Sequence 31269, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31269
;   LENGTH: 478
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(478)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31269

  Query Match             14.7%;  Score 440.8;  DB 10;  Length 478;
  Best Local Similarity   99.5%;  Pred. No. 2.3e-126;
  Matches  442;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1908 TTTGACTTTTATTATACTTTTACCTTAACACTAAGCTCCAGAAACCCTATGCTATTCTCT 1967
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         34 TCTGACTTTTATTATACTTTTACCTTAACACTAAGCTCCAGAAACCCTATGCTATTCTCT 93

Qy       1968 GTACACTCAGTTTGCTCCATGCTTTGGAATCTTTCCTCTCTCTGGGGTTCCATCTCTCCT 2027
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 GTACACTCAGTTTGCTCCATGCTTTGGAATCTTTCCTCTCTCTGGGGTTCCATCTCTCCT 153

Qy       2028 TGTGTGCCTTTTAATTCCTACTTCAGATTTCACTTTAAGTATCATCTTCCCTGGGAAGTT 2087
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 TGTGTGCCTTTTAATTCCTACTTCAGATTTCACTTTAAGTATCATCTTCCCTGGGAAGTT 213

Qy       2088 TTCCCAGACTCTCCCCACTGCCTTTGCTGAGCTGATCCTGTGTGTTTTGCTGCTGAATTT 2147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TTCCCAGACTCTCCCCACTGCCTTTGCTGAGCTGATCCTGTGTGTTTTGCTGCTGAATTT 273

Qy       2148 TGGTGTATGATCACCCTCCTTTAGCCATCTCTCTGATGGCTGTGAGCTCCATGTGGTCAG 2207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 TGGTGTATGATCACCCTCCTTTAGCCATCTCTCTGATGGCTGTGAGCTCCATGTGGTCAG 333

Qy       2208 TACCATTATCTGGCCCATCCTGGGACCCAGAGAAAGCACAAAGGAGGGCGTAACCCGGTC 2267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TACCATTATCTGGCCCATCCTGGGACCCAGAGAAAGCACAAAGGAGGGCGTAACCCGGTC 393

Qy       2268 TCACCAAATGCCTGTTGATTGATTGGACAAAGGTGACCGCGAGTGGTTCTGGGACTTGGC 2327
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        394 TCACCAAATGCCTGTTGATTGATTGGACAAAGGTGACCGCGAGTGGTTCTGTGACTTGGC 453

Qy       2328 TACGGGAACCATGAAGGAGCGTTC 2351
              ||||||||||||||||||||||||
Db        454 TACGGGAACCATGAAGGAGCGTTC 477

RESULT 7
US-10-125-237-19
; Sequence 19, Application US/10125237
; Publication No. US20030022329A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhang, Jie
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;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: No. US20030022329A1el Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 791CIP2ADIV
;  CURRENT APPLICATION NUMBER: US/10/125,237
;  CURRENT FILING DATE:  2002-04-17
;  PRIOR APPLICATION NUMBER: 09/668,317
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: 09/552,929
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 91
;  SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 19
;   LENGTH: 1631
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (71)..(1459)
US-10-125-237-19

  Query Match              7.3%;  Score 217.6;  DB 15;  Length 1631;
  Best Local Similarity   98.2%;  Pred. No. 3.4e-56;
  Matches  220;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2290 TTGGACAAAGGTGACCGCGAGTGGTTCTGGGACTTGGCTACGGGAACCATGAAGGAGCGT 2349
              ||   | |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 TTCTTCCAAGGTGACCGCGAGTGGTTCTGGGACTTGGCTACGGGAACCATGAAGGAGCGT 610

Qy       2350 TCCTGGCCAGCTGTTGGGAACTGCTCCTCTGCCCTGAGATGGCTGGGCCGCTACTACTGC 2409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 TCCTGGCCAGCTGTTGGGAACTGCTCCTCTGCCCTGAGATGGCTGGGCCGCTACTACTGC 670

Qy       2410 TTCCAGGGTAACCAATTCCTGCGCTTCGACCCTGTCAGGGGAGAGGTGCCTCCCAGGTAC 2469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        671 TTCCAGGGTAACCAATTCCTGCGCTTCGACCCTGTCAGGGGAGAGGTGCCTCCCAGGTAC 730

Qy       2470 CCGCGGGATGTCCGAGACTACTTCATGCCCTGCCCTGGCAGAGG 2513
              ||||||||||||||||||||||||||||||||||||||||||||
Db        731 CCGCGGGATGTCCGAGACTACTTCATGCCCTGCCCTGGCAGAGG 774

RESULT 8
US-10-105-891-19
; Sequence 19, Application US/10105891
; Publication No. US20030073099A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: No. US20030073099A1el Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 791CIP2A
;  CURRENT APPLICATION NUMBER: US/10/105,891
;  CURRENT FILING DATE:  2002-03-25
;  PRIOR APPLICATION NUMBER: 09/668,317
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: 09/552,929
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 91
;  SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 19
;   LENGTH: 1631
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (71)..(1459)
US-10-105-891-19

  Query Match             7.3%;  Score 217.6;  DB 15;  Length 1631;
  Best Local Similarity   98.2%;  Pred. No. 3.4e-56;
  Matches  220;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2290 TTGGACAAAGGTGACCGCGAGTGGTTCTGGGACTTGGCTACGGGAACCATGAAGGAGCGT 2349
              ||   | |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 TTCTTCCAAGGTGACCGCGAGTGGTTCTGGGACTTGGCTACGGGAACCATGAAGGAGCGT 610

Qy       2350 TCCTGGCCAGCTGTTGGGAACTGCTCCTCTGCCCTGAGATGGCTGGGCCGCTACTACTGC 2409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 TCCTGGCCAGCTGTTGGGAACTGCTCCTCTGCCCTGAGATGGCTGGGCCGCTACTACTGC 670

Qy       2410 TTCCAGGGTAACCAATTCCTGCGCTTCGACCCTGTCAGGGGAGAGGTGCCTCCCAGGTAC 2469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        671 TTCCAGGGTAACCAATTCCTGCGCTTCGACCCTGTCAGGGGAGAGGTGCCTCCCAGGTAC 730

Qy       2470 CCGCGGGATGTCCGAGACTACTTCATGCCCTGCCCTGGCAGAGG 2513
              ||||||||||||||||||||||||||||||||||||||||||||
Db        731 CCGCGGGATGTCCGAGACTACTTCATGCCCTGCCCTGGCAGAGG 774


RESULT 9
US-09-918-995-32181
; Sequence 32181, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32181
;    LENGTH: 473
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (1)...(473)
;    OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32181

  Query Match             5.6%;  Score 167.4;  DB 10;  Length 473;
  Best Local Similarity   93.0%;  Pred. No. 6.9e-41;
  Matches  174;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy       2327 CTACGGGAACCATGAAGGAGCGTTCCTGGCCAGCTGTTGGGAACTGCTCCTCTGCCCTGA 2386
              |||||  |   | |    |   ||||||||||||||||||||||||||||||||||||||
Db         12 CTACGCTAGNGACGNGCAATTCTTCCTGGCCAGCTGTTGGGAACTGCTCCTCTGCCCTGA 71

Qy       2387 GATGGCTGGGCCGCTACTACTGCTTCCAGGGTAACCAATTCCTGCGCTTCGACCCTGTCA 2446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 GATGGCTGGGCCGCTACTACTGCTTCCAGGGTAACCAATTCCTGCGCTTCGACCCTGTCA 131

Qy       2447 GGGGAGAGGTGCCTCCCAGGTACCCGCGGGATGTCCGAGACTACTTCATGCCCTGCCCTG 2506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GGGGAGAGGTGCCTCCCAGGTACCCGCGGGATGTCCGAGACTACTTCATGCCCTGCCCTG 191

Qy       2507 GCAGAGG 2513
              |||||||
Db        192 GCAGAGG 198
```

```
RESULT 10
US-09-900-448-1
; Sequence 1, Application US/09900448
; Publication No. US20030220488A1
; GENERAL INFORMATION:
;  APPLICANT: CECCARDI, Toni et al.
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001272
;  CURRENT APPLICATION NUMBER: US/09/900,448
;  CURRENT FILING DATE:  2001-07-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;    LENGTH: 3186
;    TYPE: DNA
;    ORGANISM: Human
US-09-900-448-1

  Query Match             5.4%;  Score 161.4;  DB 11;  Length 3186;
  Best Local Similarity   96.5%;  Pred. No. 2e-38;
  Matches  165;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1430 CTTTTGAATGCAGGGGGACAAAGTCTGGGTATACCCTCCTGAAAAGAAGGAGAAAGGATA 1489
              ||||   ||  |||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 CTTTCTGATCAAGGGGGACAAAGTCTGGGTATACCCTCCTGAAAAGAAGGAGAAAGGATA 397

Qy       1490 CCCAAAGTTGCTCCAAGATGAATTTCCTGGAATCCCATCCCCACTGGATGCAGCTGTGGA 1549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 CCCAAAGTTGCTCCAAGATGAATTTCCTGGAATCCCATCCCCACTGGATGCAGCTGTGGA 457

Qy       1550 ATGTCACCGTGGAGAATGTCAAGCTGAAGGCGTCCTCTTCTTCCAAGGTCA 1600
              |||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        458 ATGTCACCGTGGAGAATGTCAAGCTGAAGGCGTCCTCTTCTTCCAAGGCCA 508


RESULT 11
US-10-175-523-84
; Sequence 84, Application US/10175523
; Publication No. US20030096264A1
; GENERAL INFORMATION:
;  APPLICANT: Brockman, Jeffrey
;  APPLICANT:  Evans, David
;  APPLICANT:  Hook, Derek
;  APPLICANT:  Klimczak, Leszek
;  APPLICANT:  Laeng, Pascal
;  APPLICANT:  Palfreyman, Michael
;  APPLICANT:  Rajan, Prithi
;  TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
;  FILE REFERENCE: 3235/1J795-US3
;  CURRENT APPLICATION NUMBER: US/10/175,523
;  CURRENT FILING DATE:  2002-06-18
;  PRIOR APPLICATION NUMBER: US 60/299,151
;  PRIOR FILING DATE: 2001-06-18
;  PRIOR APPLICATION NUMBER: US 60/317,828
;  PRIOR FILING DATE: 2001-09-07
;  PRIOR APPLICATION NUMBER: US 60/325,150
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US 60/333,047
;  PRIOR FILING DATE: 2001-11-14
;  PRIOR APPLICATION NUMBER: US 60/349,936
;  PRIOR FILING DATE: 2002-01-18
;  PRIOR APPLICATION NUMBER: US 60/361,834
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
;    LENGTH: 1516
;    TYPE: DNA
;    ORGANISM: Rattus norvegicus
US-10-175-523-84
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  Query Match             5.3%;  Score 159.6;  DB 15;  Length 1516;
  Best Local Similarity   76.8%;  Pred. No. 4.4e-38;
  Matches  195;  Conservative    0;  Mismatches   59;  Indels    0;  Gaps    0;

Qy       2290 TTGGACAAAGGTGACCGCGAGTGGTTCTGGGACTTGGCTACGGGAACCATGAAGGAGCGT 2349
              ||   | ||||| ||||| |||||||||||||||| || ||  |||||   ||||| |||
Db        532 TTCTTCCAAGGTAACCGCAAGTGGTTCTGGGACTTTGCCACAAGAACCCAAAAGGAACGT 591

Qy       2350 TCCTGGCCAGCTGTTGGGAACTGCTCCTCTGCCCTGAGATGGCTGGGCCGCTACTACTGC 2409
              |||||||| ||||||||||| ||| |  | ||| |||| ||||| |  ||||||||||||
Db        592 TCCTGGCCTGCTGTTGGGAATTGCACTGCGGCCTTGAGGTGGCTTGAACGCTACTACTGC 651

Qy       2410 TTCCAGGGTAACCAATTCCTGCGCTTCGACCCTGTCAGGGGAGAGGTGCCTCCCAGGTAC 2469
              |||||||||||| | |||||| | ||  |||| ||||  ||||||||||||||||| |||
Db        652 TTCCAGGGTAACAAGTTCCTGAGATTTAACCCCGTCACAGGAGAGGTGCCTCCCAGATAC 711

Qy       2470 CCGCGGGATGTCCGAGACTACTTCATGCCCTGCCCTGGCAGAGGTGAGAAAGCCCTAGCA 2529
              || | ||||| ||| |||||||||||  ||||||||||||||||  |       |||  |
Db        712 CCTCTGGATGCCCGTGACTACTTCATATCCTGCCCTGGCAGAGGCCATGGTAAACTAAGA 771

Qy       2530 CTTGAGACCTGTCA 2543
                ||  ||   |||
Db        772 AATGGAACTGCTCA 785

RESULT 12
US-10-316-253-39
; Sequence 39, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
;  APPLICANT: The Procter & Gamble Company
;  APPLICANT:  Peters, Kevin
;  APPLICANT:  Thompson, Larry
;  APPLICANT:  Wang, Feng
;  APPLICANT:  Greis, Kenneth
;  TITLE OF INVENTION: Angiogenesis Modulating Proteins
;  FILE REFERENCE: 8865M
;  CURRENT APPLICATION NUMBER: US/10/316,253
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: US 60/355,295
;  PRIOR FILING DATE: 2002-02-08
;  NUMBER OF SEQ ID NOS: 308
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
;   LENGTH: 1516
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (55)..(1437)
;   OTHER INFORMATION:
US-10-316-253-39

  Query Match             5.3%;  Score 159.6;  DB 15;  Length 1516;
  Best Local Similarity   76.8%;  Pred. No. 4.4e-38;
  Matches  195;  Conservative    0;  Mismatches   59;  Indels    0;  Gaps    0;

Qy       2290 TTGGACAAAGGTGACCGCGAGTGGTTCTGGGACTTGGCTACGGGAACCATGAAGGAGCGT 2349
              ||   | ||||| ||||| |||||||||||||||| || ||  |||||   ||||| |||
Db        532 TTCTTCCAAGGTAACCGCAAGTGGTTCTGGGACTTTGCCACAAGAACCCAAAAGGAACGT 591

Qy       2350 TCCTGGCCAGCTGTTGGGAACTGCTCCTCTGCCCTGAGATGGCTGGGCCGCTACTACTGC 2409
              |||||||| ||||||||||| ||| |  | ||| |||| ||||| |  ||||||||||||
Db        592 TCCTGGCCTGCTGTTGGGAATTGCACTGCGGCCTTGAGGTGGCTTGAACGCTACTACTGC 651

Qy       2410 TTCCAGGGTAACCAATTCCTGCGCTTCGACCCTGTCAGGGGAGAGGTGCCTCCCAGGTAC 2469
              |||||||||||| | |||||| | ||  |||| ||||  ||||||||||||||||| |||
Db        652 TTCCAGGGTAACAAGTTCCTGAGATTTAACCCCGTCACAGGAGAGGTGCCTCCCAGATAC 711

Qy       2470 CCGCGGGATGTCCGAGACTACTTCATGCCCTGCCCTGGCAGAGGTGAGAAAGCCCTAGCA 2529
              || | ||||| ||| |||||||||||  ||||||||||||||||  |       |||  |
Db        712 CCTCTGGATGCCCGTGACTACTTCATATCCTGCCCTGGCAGAGGCCATGGTAAACTAAGA 771
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Qy       2530 CTTGAGACCTGTCA 2543
                ||  ||   |||
Db        772 AATGGAACTGCTCA 785

RESULT 13
US-09-960-352-2954
; Sequence 2954, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 2954
;   LENGTH: 367
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 13-LIB34-011-Q1-E1-D1
US-09-960-352-2954

  Query Match             5.3%;  Score 157.8;  DB 9;  Length 367;
  Best Local Similarity   79.8%;  Pred. No. 5.8e-38;
  Matches  186;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy       2281 GTTGATTGATTGGACAAAGGTGACCGCGAGTGGTTCTGGGACTTGGCTACGGGAACCATG 2340
              | ||  |  ||   | ||||  ||| |  |||||||||||||||  ||||   ||||||
Db         56 GGTGTCTTCTTCTTCCAAGGCAACCACACGTGGTTCTGGGACTTCTCTACAAAAACCATA 115

Qy       2341 AAGGAGCGTTCCTGGCCAGCTGTTGGGAACTGCTCCTCTGCCCTGAGATGGCTGGGCCGC 2400
              ||| | |||||||||||||| ||||||||||||||||| ||| |  |||||||   ||||
Db        116 AAGAAACGTTCCTGGCCAGCCGTTGGGAACTGCTCCTCGGCCATACGATGGCTCAACCGC 175

Qy       2401 TACTACTGCTTCCAGGGTAACCAATTCCTGCGCTTCGACCCTGTCAGGGGAGAGGTGCCT 2460
              ||||||||||||| ||||||| ||||||||||||||||||| |||| |||||| |||  |
Db        176 TACTACTGCTTCCGGGGTAACAAATTCCTGCGCTTCGACCCCGTCACGGGAGAAGTGAAT 235

Qy       2461 CCCAGGTACCCGCGGGATGTCCGAGACTACTTCATGCCCTGCCCTGGCAGAGG 2513
               |||  || || |||||||||||||| ||||| ||| ||||||||  ||||||
Db        236 TCCACTTATCCTCGGGATGTCCGAGATTACTTTATGTCCTGCCCTAACAGAGG 288

RESULT 14
US-09-960-352-14163
; Sequence 14163, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 14163
;   LENGTH: 422
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 60-LIB34-071-Q1-E1-G12
US-09-960-352-14163

  Query Match             5.3%;  Score 157.8;  DB 9;  Length 422;
  Best Local Similarity   79.8%;  Pred. No. 6.4e-38;
  Matches  186;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy        2281 GTTGATTGATTGGACAAAGGTGACCGCGAGTGGTTCTGGGACTTGGCTACGGGAACCATG 2340
               | ||  |  ||   | ||||  ||| |  |||||||||||||||  ||||   ||||||
Db         156 GGTGTCTTCTTCTTCCAAGGCAACCACACGTGGTTCTGGGACTTCTCTACAAAAACCATA 215

Qy        2341 AAGGAGCGTTCCTGGCCAGCTGTTGGGAACTGCTCCTCTGCCCTGAGATGGCTGGGCCGC 2400
               ||| | |||||||||||||| ||||||||||||||||| ||| |  |||||||   ||||
Db         216 AAGAAACGTTCCTGGCCAGCCGTTGGGAACTGCTCCTCGGCCATACGATGGCTCAACCGC 275

Qy        2401 TACTACTGCTTCCAGGGTAACCAATTCCTGCGCTTCGACCCTGTCAGGGGAGAGGTGCCT 2460
               ||||||||||||| ||||||| ||||||||||||||||||| |||| |||||| |||  |
Db         276 TACTACTGCTTCCGGGGTAACAAATTCCTGCGCTTCGACCCCGTCACGGGAGAAGTGAAT 335

Qy        2461 CCCAGGTACCCGCGGGATGTCCGAGACTACTTCATGCCCTGCCCTGGCAGAGG 2513
                |||  || || |||||||||||||| ||||| ||| ||||||||  ||||||
Db         336 TCCACTTATCCTCGGGATGTCCGAGATTACTTTATGTCCTGCCCTAACAGAGG 388


RESULT 15
US-09-960-352-421
; Sequence 421, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 421
;   LENGTH: 393
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 02-LIB34-048-Q1-E1-A5
US-09-960-352-421

  Query Match             5.2%;  Score 154.6;  DB 9;  Length 393;
  Best Local Similarity   79.0%;  Pred. No. 6.1e-37;
  Matches  184;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy        2281 GTTGATTGATTGGACAAAGGTGACCGCGAGTGGTTCTGGGACTTGGCTACGGGAACCATG 2340
               | ||  |  ||   | ||||  ||| |  |||||||||||||||  ||||   ||||||
Db         135 GGTGTCTTCTTCTTCCAAGGCAACCACACGTGGTTCTGGGACTTCTCTACAAAAACCATA 194

Qy        2341 AAGGAGCGTTCCTGGCCAGCTGTTGGGAACTGCTCCTCTGCCCTGAGATGGCTGGGCCGC 2400
               ||| | |||||||||||||| ||||||||||||||||| ||| |  |||||||   ||||
Db         195 AAGAAACGTTCCTGGCCAGCCGTTGGGAACTGCTCCTCGGCCATACGATGGCTCAACCGC 254

Qy        2401 TACTACTGCTTCCAGGGTAACCAATTCCTGCGCTTCGACCCTGTCAGGGGAGAGGTGCCT 2460
               ||||||||||||| ||||||| ||||||||||||||||||| |||| |||||| |||  |
Db         255 TACTACTGCTTCCGGGGTAACAAATTCCTGCGCTTCGACCCCGTCACGGGAGAAGTGAAT 314

Qy        2461 CCCAGGTACCCGCGGGATGTCCGAGACTACTTCATGCCCTGCCCTGGCAGAGG 2513
                |||  || || |||||||||||||| ||| | ||| ||||||||  |||| |
Db         315 TCCACTTATCCTCGGGATGTCCGAGATTACGTTATGTCCTGCCCTAACAGATG 367


Search completed: June  8, 2004, 23:18:04
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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2004  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         June  8, 2004, 17:11:50 ; Search time 142 Seconds
                                           (without alignments)
                                          11724.315 Million cell updates/sec

Title:          US-09-900-448-3_COPY_3001_6000
Perfect score:  3000
Sequence:       1 tcttagttctacaccgctct..........ctccattgtcatcactgtgt 3000

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters:       1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 2:  /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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                 6:  /cgn2_6/ptodata/2/ina/backfiles1.seq:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result              Query
  No.     Score     Match Length DB  ID                          Description
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     1     81.8      2.7    7218  1  US-08-232-463-14            Sequence 14, Appl
c    2     70.8      2.4    7218  1  US-08-232-463-14            Sequence 14, Appl
     3     58.4      1.9    1128  4  US-09-205-258-182           Sequence 182, App
     4     48.8      1.6     619  4  US-09-489-847-58            Sequence 58, Appl
     5       48      1.6   22976  4  US-09-269-939A-19           Sequence 19, Appl
     6     47.6      1.6   44453  4  US-09-146-053-5             Sequence 5, Appli
     7       47      1.6   28720  4  US-09-341-587-7             Sequence 7, Appli
     8     46.2      1.5   21721  4  US-09-269-939A-41           Sequence 41, Appl
     9     45.6      1.5     191  4  US-09-621-976-9448          Sequence 9448, Ap
    10     44.8      1.5   23187  4  US-09-499-522-1             Sequence 1, Appli
    11     43.8      1.5     300  3  US-09-157-177-118           Sequence 118, App
    12     43.8      1.5    6063  1  US-08-195-744-4             Sequence 4, Appli
    13     43.8      1.5    6063  2  US-08-788-279-4             Sequence 4, Appli
c   14     43.2      1.4     819  4  US-09-369-247-44            Sequence 44, Appl
c   15     43.2      1.4     941  4  US-09-205-258-13            Sequence 13, Appl
c   16     43.2      1.4     941  4  US-09-205-258-218           Sequence 218, App
    17     43.2      1.4    3634  3  US-09-166-186-1             Sequence 1, Appli
    18     43.2      1.4    3634  3  US-09-313-932-1             Sequence 1, Appli
    19     43.2      1.4    3634  3  US-09-109-663-34            Sequence 34, Appl
c   20     43.2      1.4  392000  4  US-10-027-983-11            Sequence 11, Appl
c   21       43      1.4    2426  4  US-10-011-858-1             Sequence 1, Appli
    22     42.8      1.4   38653  4  US-09-922-445-1             Sequence 1, Appli
c   23     42.2      1.4  161652  4  US-09-497-855A-40           Sequence 40, Appl
    24     41.6      1.4  246240  2  US-08-724-394A-20           Sequence 20, Appl
    25     41.6      1.4  246240  2  US-08-724-394A-21           Sequence 21, Appl
    26     41.6      1.4  246240  2  US-08-724-394A-22           Sequence 22, Appl
    27     41.4      1.4      78  3  US-09-030-156-20            Sequence 20, Appl
    28     41.4      1.4      78  4  US-09-645-757-20            Sequence 20, Appl
c   29     41.4      1.4    3601  3  US-09-017-631-23            Sequence 23, Appl
c   30     41.4      1.4    3602  2  US-08-883-795A-33           Sequence 33, Appl
c   31     41.4      1.4    3602  3  US-09-018-138-1             Sequence 1, Appli
c   32     41.4      1.4  162450  4  US-09-345-882-1             Sequence 1, Appli
    33     40.8      1.4  392000  4  US-10-027-983-11            Sequence 11, Appl
c   34     40.6      1.4    2714  4  US-09-023-655-928           Sequence 928, App
    35     40.2      1.3    4267  4  US-09-023-655-1379          Sequence 1379, Ap
    36       40      1.3      74  3  US-09-030-156-19            Sequence 19, Appl
    37       40      1.3      74  4  US-09-645-757-19            Sequence 19, Appl
    38       40      1.3     457  4  US-09-621-976-15457         Sequence 15457, A
    39       40      1.3     700  4  US-09-236-097-8             Sequence 8, Appli
    40     39.8      1.3      72  3  US-09-358-972-156           Sequence 156, App
    41     39.8      1.3      72  4  US-09-383-316-50            Sequence 50, Appl
c   42     39.8      1.3     289  3  US-09-007-005-17            Sequence 17, Appl
c   43     39.8      1.3     289  3  US-09-244-796-17            Sequence 17, Appl
    44     39.8      1.3     832  4  US-09-621-976-2813          Sequence 2813, Ap
    45     39.6      1.3     502  4  US-09-148-545-15            Sequence 15, Appl

                              ALIGNMENTS

RESULT 1
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             2.7%;  Score 81.8;  DB 1;  Length 7218;
  Best Local Similarity   4.3%;  Pred. No. 8.2e-14;
  Matches   17;  Conservative  245;  Mismatches  137;  Indels    0;  Gaps    0;

Qy       1794 TGTAATTCTGTGTGAATAGTCCCTCATTGTTCCCCATGACCCTTAGGACAAATCTACCCT 1853
              ||  ||:::  :  :    :   :::::: :: :::::: :   :::::      :    ::: ::::
Db       1061 TGCGATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1120

Qy       1854 CTTTAGTCTTACATACAAGTCTCTCCATGGCCAAATCCCTATTGGCCCTTCAGCTTTGAC 1913
              ::::  :::: :  :  :    ::::::: :   ::    ::::: ::  ::::::  ::::   :
Db       1121 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1180

Qy       1914 TTTTATTATACTTTTACCTTAACACTAAGCTCCAGAAACCCTATGCTATTCTCTGTACAC 1973
              :::: :: : ::::: ::::   : ::    ::::         :::: : :: :::::: :  : :
Db       1181 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1240

Qy       1974 TCAGTTTGCTCCATGCTTTGGAATCTTTCCTCTCTCTGGGGTTCCATCTCTCCTTGTGTG 2033
              ::   ::: :::: : ::::      ::::::::::::::      :::: ::::::::: :  :
Db       1241 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1300

Qy       2034 CCTTTTAATTCCTACTTCAGATTTCACTTTAAGTATCATCTTCCCTGGGAAGTTTTCCCA 2093
              ::::::   ::::: ::::    :::: ::::    : :: ::::::::       :::::::
Db       1301 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1360

Qy       2094 GACTCTCCCCACTGCCTTTGCTGAGCTGATCCTGTGTGTTTTGCTGCTGAATTTTGGTGT 2153
                ::::::::: :: ::::: ::    ::  :::: : : :::: :: ::    ::::  : :
Db       1361 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1420

Qy       2154 ATGATCACCCTCCTTTAGCCATCTCTCTGATGGCTGTGA 2192
               :   :: :::::::: || |  |   |||    ||   || | |
Db       1421 YYYYYYYYYYYYYYYGTACCAAATTCTTCTATCTCTTTAA 1459


RESULT 2
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;   INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             2.4%;  Score 70.8;  DB 1;  Length 7218;
  Best Local Similarity   9.5%;  Pred. No. 1.8e-10;
  Matches   45;  Conservative  237;  Mismatches  194;  Indels    0;  Gaps    0;

Qy       1003 AGTGAAAGACAGAGTCTTGTTATCCTCAGTGCCTCTCACAATGCCTGGCATATAGTAGTT 1062
              |||    | | |   | | |||     | ||| ||     |   | ||    ||  |       ||
Db       1513 AGTTTCAAAAAACGGCATGTAGGCATCACTGTAATTACCTATCTATGCAAGTAGTTAAAG 1454

Qy       1063 ATTCAGTGACTGTTTCTTGGATGAATGAATGAATGAATAAATAAATGAAGAAATGAATGA 1122
              |    ||         ||  |    :: ::: ::: ::: ::: ::: ::: ::::::: ::: ::
Db       1453 AGATAGAAGAATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1394

Qy       1123 AGAAATAACGTATGGGTGATTGCAGGATGAACAGTTGTGGATATGTTTGTCAACACTGAT 1182
              ::::: :: : : ::: ::    : :::: ::: ::    : ::: : :     :   :: :  ::
Db       1393 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1334

Qy       1183 AGTGTTGCAGATAAATGTGCCACAGGAGTGTCTGGGTACAGAGCTAGAGGCATGTGTGTT 1242
              :: :   : ::: ::: : :    : ::::: :     ::: : ::::    ::::: : : : :
Db       1333 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1274

Qy       1243 ATAGTAATAGTGACTGGATTTGCACAAACTGAGAGTGTGTAATGTGCAAAAGGACAGCAC 1302
              : :: :: :: ::   :::      : : :::    ::::: : : :: : : ::::::: :: :
Db       1273 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1214

Qy       1303 ATTGTTGTCCACAGATGGACTGAGAATGTGTAGGGCCACAGAAGGATATCGTATAAGCAC 1362
              :  :  :     : ::: :::    ::::: : : ::::   : ::::::: :    : : ::: :
Db       1213 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1154

Qy       1363 AGTAGATAAAAAATGTGTGTAAATGCAGAGTGGCAGTATCTGGGGATGCACAGTCAAAAA 1422
              :: ::: :::::: : : : ::: : :::: :: :: :    ::::: : : ::   :::::
Db       1153 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1094

Qy       1423 GAGAGTACTTTTGAATGCAGGGGGACAAAGTCTGGGTATACCCTCCTGAAAAGAAG 1478
              ::::: :       ::: : ::::::: :|    |   | |     |  ||||  |   |||
Db       1093 RRRRRRRRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCTCGACCTGCAGCCAAG 1038


RESULT 3
US-09-205-258-182
; Sequence 182, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
;  APPLICANT: Young et al.
;  TITLE OF INVENTION: 207 Human Secreted Proteins
;  FILE REFERENCE: PZ007P1
;  CURRENT APPLICATION NUMBER: US/09/205,258
;  CURRENT FILING DATE: 1998-12-04
;  EARLIER APPLICATION NUMBER: PCT/US98/11422
;  EARLIER FILING DATE: 1998-06-04
;  EARLIER APPLICATION NUMBER: 60/048,885
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,375
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,881
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,880
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,896
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,020
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,876
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,895
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,884
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,894
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,971
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,964
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,882
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,899
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,893
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,900
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,901
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,892
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,915
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,019
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,970
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,972
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,916
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,373
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,875
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,374
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,917
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,949
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,974
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,883
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,897
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,898
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,962
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,963
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,877
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,878
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/070,923
;  EARLIER FILING DATE: 1997-12-18
;  EARLIER APPLICATION NUMBER: 60/092,921
;  EARLIER FILING DATE: 1998-07-15
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 1227
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 182
;   LENGTH: 1128
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-205-258-182

  Query Match             1.9%;  Score 58.4;  DB 4;  Length 1128;
  Best Local Similarity   74.0%;  Pred. No. 3.1e-07;
  Matches   74;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;
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Qy       1017 TCTTGTTATCCTCAGTGCCTCTCACAATGCCTGGCATATAGTAGTTATTCAGTGACTGTT 1076
              ||||  ||||| |||  |||  ||||   ||||| || | |||| |  ||||| | |||
Db        905 TCTTCCTATCCCCAGAACCTTGCACAGATCCTGGAATGTGGTAGGTGCTCAGTAAATGTG 964

Qy       1077 TCTTGGATGAATGAATGAATGAATAAATAAATGAAGAAAT 1116
              | ||| || ||||||||||||||| || |||||||  |||
Db        965 TGTTGAATAAATGAATGAATGAATGAACAAATGAATGAAT 1004


RESULT 4
US-09-489-847-58
; Sequence 58, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al
;  TITLE OF INVENTION: 98 Human Secreted Proteins
;  FILE REFERENCE: PZ031P1
;  CURRENT APPLICATION NUMBER: US/09/489,847
;  CURRENT FILING DATE: 2000-01-24
;  EARLIER APPLICATION NUMBER: PCT/US99/17130
;  EARLIER FILING DATE: 1999-07-29
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  EARLIER APPLICATION NUMBER: 60/095,486
;  EARLIER FILING DATE: 1998-08-05
;  EARLIER APPLICATION NUMBER: 60/096,319
;  EARLIER FILING DATE: 1998-08-12
;  EARLIER APPLICATION NUMBER: 60/095,454
;  EARLIER FILING DATE: 1998-08-06
;  EARLIER APPLICATION NUMBER: 60/095,455
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 376
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
;   LENGTH: 619
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (526)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (619)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-489-847-58

  Query Match             1.6%;  Score 48.8;  DB 4;  Length 619;
  Best Local Similarity   63.2%;  Pred. No. 0.00017;
  Matches   74;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy       1014 GAGTCTTGTTATCCTCAGTGCCTCTCACAATGCCTGGCATATAGTAGTTATTCAGTGACT 1073
              || | ||  |||   ||||||||  |    |||||||||  ||| |   | ||| | | |
Db        498 GAATTTTTGTATTAACAGTGCCTGGCTTNGTGCCTGGCACCTAGAAAGCACTCAATAAAT 557

Qy       1074 GTTTCTTGGATGAATGAATGAATGAATAAATAAATGAAGAAATGAATGAAGAAATAA 1130
              |||| ||  |||||  ||  ||  || ||| |||  || |||  ||  || ||| ||
Db        558 GTTTGTTTAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 614


RESULT 5
US-09-269-939A-19
; Sequence 19, Application US/09269939A
; Patent No. 6635431
; GENERAL INFORMATION:
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Yen-Potin, Frances
;  TITLE OF INVENTION:  LSR Receptor, Its Activity, Its Cloning and Its Application To
;  TITLE OF INVENTION:  The Diagnosis Prevention And/or Treatment of Obesity and
;  TITLE OF INVENTION:  Related Risks or Complications
;  FILE REFERENCE:  GENSET.035APC
;  CURRENT APPLICATION NUMBER: US/09/269,939A
;  CURRENT FILING DATE:  1999-05-28
;  PRIOR APPLICATION NUMBER:  FR 97/10088
;  PRIOR FILING DATE:  1997-08-06
;  PRIOR APPLICATION NUMBER:  FR 98/05032
;  PRIOR FILING DATE:  1998-04-22
;  NUMBER OF SEQ ID NOS:  41
;  SOFTWARE:  Patent.pm
; SEQ ID NO 19
;   LENGTH: 22976
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 1898..2253
;   NAME/KEY: exon
;   LOCATION: 3437..3781
;   NAME/KEY: exon
;   LOCATION: 12065..12184
;   NAME/KEY: exon
;   LOCATION: 15045..15101
;   NAME/KEY: exon
;   LOCATION: 15666..15812
;   NAME/KEY: exon
;   LOCATION: 19479..19652
;   NAME/KEY: exon
;   LOCATION: 19799..19858
;   NAME/KEY: exon
;   LOCATION: 19956..20087
;   NAME/KEY: exon
;   LOCATION: 20229..20854
;   NAME/KEY: exon
;   LOCATION: 20944..21094
;   NAME/KEY: Misc_Feature
;   LOCATION: 19956..19958
;   OTHER INFORMATION: Potential variant splicing site AAG
US-09-269-939A-19

  Query Match             1.6%;  Score 48;  DB 4;  Length 22976;
  Best Local Similarity   68.6%;  Pred. No. 0.0036;
  Matches   81;  Conservative    0;  Mismatches   35;  Indels    2;  Gaps    1;

Qy       1020 TGTTATCCTCAGTGCCTCTCACAATGCCTGGCATATAGTAGTTATTCAGTGACTGT--TT 1077
              || |||||   ||| |||  | | ||||| | | ||||  | || ||||| | | |  ||
Db       9755 TGGTATCCCAGGTGTCTCAAATACTGCCTAGAACATAGGTGGTACTCAGTAATTATTGTT 9814

Qy       1078 CTTGGATGAATGAATGAATGAATAAATAAATGAAGAAATGAATGAAGAAATAACGTAT 1135
                 |||||||||||||||||||| ||| ||||||  || ||| |||  ||    || |
Db       9815 GAAGGATGAATGAATGAATGAATGAATGAATGAAAGAAAGAAAGAAATGTGTCT 9872

RESULT 6
US-09-146-053-5
; Sequence 5, Application US/09146053A
; Patent No. 6399349
; GENERAL INFORMATION:
;  APPLICANT: Ryan, James W.
;  APPLICANT: Sprinkle, Terry Joe Curtis
;  APPLICANT: Venema, Richard C.
;  TITLE OF INVENTION: Human Aminopeptidase P Gene
;  FILE REFERENCE: MCG103
;  CURRENT APPLICATION NUMBER: US/09/146,053A
;  CURRENT FILING DATE: 1998-09-02
;  EARLIER APPLICATION NUMBER: 60/057,854
;  EARLIER FILING DATE: 1997-09-02
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 44453
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-146-053-5

  Query Match             1.6%;  Score 47.6;  DB 4;  Length 44453;
  Best Local Similarity   59.7%;  Pred. No. 0.0074;
  Matches   80;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    0;

Qy       1023 TATCCTCAGTGCCTCTCACAATGCCTGGCATATAGTAGTTATTCAGTGACTGTTTCTTGG 1082
              || ||  ||  |||  || | ||| ||||| |||| ||     |||  | |||||  ||
Db      30421 TACCCCTAGGACCTAGCAAAGTGCTTGGCACATAGCAGGCGCCCAGCAAGTGTTTTATGA 30480

Qy       1083 ATGAATGAATGAATGAATAAATAAATGAAGAAATGAATGAAGAAATAACGTATGGGTGAT 1142
              |||||||||| ||||||| |||   |  |   |   |   |   |  | | |||| || |
Db      30481 ATGAATGAATAAATGAATGAATGCCTCTATGCAGACAGACACTGAATAAGAATGGTTGCT 30540

Qy       1143 TGCAGGATGAACAG 1156
              |||   || |  ||
Db      30541 TGCTCAATAACAAG 30554

RESULT 7
US-09-341-587-7
; Sequence 7, Application US/09341587
; Patent No. 6346606
; GENERAL INFORMATION:
;  APPLICANT: Mollenhauer, Jan
;  TITLE OF INVENTION: Protein Containing an SRCR Domain
;  FILE REFERENCE: 4121-108
;  CURRENT APPLICATION NUMBER: US/09/341,587
;  CURRENT FILING DATE: 1999-08-31
;  EARLIER APPLICATION NUMBER: PCT/DE98/00096
;  EARLIER FILING DATE: 1998-01-09
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 28720
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-341-587-7

  Query Match             1.6%;  Score 47;  DB 4;  Length 28720;
  Best Local Similarity   57.5%;  Pred. No. 0.0084;
  Matches  103;  Conservative    0;  Mismatches   75;  Indels    1;  Gaps    1;

Qy        974 TTTCTGCTTTTGTACAGTGAACTTCCTGAAGTGAAAGACAGAGTCT-TGTTATCCTCAGT 1032
              | |||  | |   | | || | |||||||||  |  | |   ||||   || | |  | |
Db      12051 TATCTTTTCTGCCAAACTGCATTTCCTGAAGGCAGGGGCCATGTCTGCCTTTTTCATAAT 12110

Qy       1033 GCCTCTCACAATGCCTGGCATATAGTAGTTATTCAGTGACTGTTTCTTGGATGAATGAAT 1092
              |  ||        |  |   | |    |   ||||   ||||||| ||| | |||| |||
Db      12111 GTATCCTTATTATCTAGCATTGTGTCTGCCTTTCAAGAACTGTTTATTGAAGGAATAAAT 12170

Qy       1093 GAATGAATAAATAAATGAAGAAATGAATGAAGAAATAACGTATGGGTGATTGCAGGATG 1151
              || ||||| ||| |||| | |||| |||||| |||||    ||   || | |||   ||
Db      12171 GAGTGAATGAATGAATGGATAAATTAATGAATAAATACATAATTACTGTTGGCATTTTG 12229

RESULT 8
US-09-269-939A-41
; Sequence 41, Application US/09269939A
; Patent No. 6635431
; GENERAL INFORMATION:
;  APPLICANT:  Bihain, Bernard
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Yen-Potin, Frances
;  TITLE OF INVENTION:  LSR Receptor, Its Activity, Its Cloning and Its Application To
;  TITLE OF INVENTION:  The Diagnosis Prevention And/or Treatment of Obesity and
;  TITLE OF INVENTION:  Related Risks or Complications
;  FILE REFERENCE:  GENSET.035APC
;  CURRENT APPLICATION NUMBER: US/09/269,939A
;  CURRENT FILING DATE:  1999-05-28
;  PRIOR APPLICATION NUMBER:  FR 97/10088
;  PRIOR FILING DATE:  1997-08-06
;  PRIOR APPLICATION NUMBER:  FR 98/05032
;  PRIOR FILING DATE:  1998-04-22
;  NUMBER OF SEQ ID NOS:  41
;  SOFTWARE:  Patent.pm
; SEQ ID NO 41
;   LENGTH: 21721
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 1898..2253
;   NAME/KEY: exon
;   LOCATION: 3438..3782
;   NAME/KEY: exon
;   LOCATION: 12064..12183
;   NAME/KEY: exon
;   LOCATION: 15049..15105
;   NAME/KEY: exon
;   LOCATION: 15670..15816
;   NAME/KEY: exon
;   LOCATION: 19486..19659
;   NAME/KEY: exon
;   LOCATION: 19806..19865
;   NAME/KEY: exon
;   LOCATION: 19963..20094
;   NAME/KEY: exon
;   LOCATION: 20236..20864
;   NAME/KEY: exon
;   LOCATION: 20954..21094
;   NAME/KEY: Misc_Feature
;   LOCATION: 715
;   OTHER INFORMATION: diverging nucleotide, G in ref genbank:AC002128
;   NAME/KEY: Misc_Feature
;   LOCATION: 1229
;   OTHER INFORMATION: diverging insertion, G in ref genbank:AC002128
;   NAME/KEY: Misc_Feature
;   LOCATION: 3676
;   OTHER INFORMATION: diverging nucleotide, T in ref genbank:AC002128
;   NAME/KEY: Misc_Feature
;   LOCATION: 5039
;   OTHER INFORMATION: diverging deletion, G in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 5118
;   OTHER INFORMATION: diverging nucleotide, C in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 7337
;   OTHER INFORMATION: diverging deletion, C in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 8294
;   OTHER INFORMATION: diverging nucleotide, G in ref genebank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 8604
;   OTHER INFORMATION: diverging nucleotide, C in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 8928
;   OTHER INFORMATION: diverging nucleotide, A in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 9021
;   OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 9851
;   OTHER INFORMATION: diverging insertion, GAATGAAA in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 9878
;   OTHER INFORMATION: diverging nucleotide, C in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 11478
;   OTHER INFORMATION: diverging mucleotide, T in ref genbank: AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 11577
;   OTHER INFORMATION: diverging deletion, C in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 11779
;   OTHER INFORMATION: diverging nucleotide, T in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 13411
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```
;   OTHER INFORMATION: diverging deletion, T in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 13538
;   OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 13896
;   OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 14912
;   OTHER INFORMATION: diverging nucleotide, A in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 16732
;   OTHER INFORMATION: diverging nucleotide, C in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 17169
;   OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 18946
;   OTHER INFORMATION: diverging deletion, G in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 19474
;   OTHER INFORMATION: diverging mucleotide, G in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 20500
;   OTHER INFORMATION: diverging deletion, G in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 20501
;   OTHER INFORMATION: diverging deletion, G in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 20502
;   OTHER INFORMATION: diverging deletion, A in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 21270
;   OTHER INFORMATION: diverging nucleotid, G in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 21356
;   OTHER INFORMATION: diverging insertion, T in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 21476
;   OTHER INFORMATION: diverging nucleotide, A in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 21588
;   OTHER INFORMATION: diverging insertion, C in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 21601
;   OTHER INFORMATION: diverging deletion, T in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 21635
;   OTHER INFORMATION: diverging insertion, G in ref genbank:AD000684
;   NAME/KEY: Misc_Feature
;   LOCATION: 19963..19965
;   OTHER INFORMATION: Potential variant splicing site AAG
;   NAME/KEY: Misc_Feature
;   LOCATION: 1..21721
;   OTHER INFORMATION: n= a,g,c or t
US-09-269-939A-41

  Query Match             1.5%;  Score 46.2;  DB 4;  Length 21721;
  Best Local Similarity   71.2%;  Pred. No. 0.012;
  Matches   74;  Conservative    0;  Mismatches   29;  Indels    1;  Gaps    1;

Qy       1020 TGTTATCCTCAGTGCCTCTCACAATGCCTGGCATATAGTAGTTATTCAGTGACTGTTTCT 1079
              || |||||   ||| |||  | | ||||| | | ||||  | || ||||| | |  || |
Db       9760 TGGTATCCCAGGTGTCTCAAATACTGCCTAGAACATAGGTGGTACTCAGT-AATTATTGT 9818

Qy       1080 TGGATGAATGAATGAATGAATAAATAAATGAAGAAATGAATGAA 1123
              || | | |||||||||||||| ||| ||||||  || ||| |||
Db       9819 TGNAAGGATGAATGAATGAATGAATGAATGAATGAAAGAAAGAA 9862


RESULT 9
US-09-621-976-9448
; Sequence 9448, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 9448
;   LENGTH: 191
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-9448

  Query Match             1.5%;  Score 45.6;  DB 4;  Length 191;
  Best Local Similarity   68.5%;  Pred. No. 0.00074;
  Matches   63;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy       1039 CACAATGCCTGGCATATAGTAGTTATTCAGTGACTGTTTCTTGGATGAATGAATGAATGA 1098
              | |  | |||| || |||||||  | ||| | | | || ||  |  ||||||||||||||
Db         88 CCCTGTTCCTGACACATAGTAGGCACTCAATAAATATTCATTAAAGGAATGAATGAATGA 147

Qy       1099 ATAAATAAATGAAGAAATGAATGAAGAAATAA 1130
              | ||| |||  || |||  ||  ||  ||| ||
Db        148 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 179


RESULT 10
US-09-499-522-1
; Sequence 1, Application US/09499522
; Patent No. 6479238
; GENERAL INFORMATION:
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Bougueleret, Lydie
;  APPLICANT: Bihain, Bernard
;  TITLE OF INVENTION: POLYMORPHIC MARKERS OF THE LSR GENE
;  FILE REFERENCE: GENSET.053AUS
;  CURRENT APPLICATION NUMBER: US/09/499,522
;  CURRENT FILING DATE: 2000-02-10
;  EARLIER APPLICATION NUMBER: US 60/119,592
;  EARLIER FILING DATE: 1999-02-10
;  EARLIER APPLICATION NUMBER: US 60/144,784
;  EARLIER FILING DATE: 1999-07-20
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: Patent.pm
; SEQ ID NO 1
;   LENGTH: 23187
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 2001..2356
;   OTHER INFORMATION: exon1
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 3540..3884
;   OTHER INFORMATION: exon2
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 12163..12282
;   OTHER INFORMATION: exon3
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 15144..15200
;   OTHER INFORMATION: exon4
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 15765..15911
;   OTHER INFORMATION: exon5
;   FEATURE:
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;   NAME/KEY: exon
;   LOCATION: 19579..19752
;   OTHER INFORMATION: exon6
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 19899..19958
;   OTHER INFORMATION: exon7
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 20056..20187
;   OTHER INFORMATION: exon8
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 20329..20957
;   OTHER INFORMATION: exon9
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 21047..21187
;   OTHER INFORMATION: exon10
;   FEATURE:
;   NAME/KEY: polyA_signal
;   LOCATION: 21168..21173
;   OTHER INFORMATION: AATAAA
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1..2000
;   OTHER INFORMATION: potential  5'regulatory  region
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 22324..23187
;   OTHER INFORMATION: homology  with  USF2  gene  in  ref:  embl  Y07661
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 523..544
;   OTHER INFORMATION: upstream amplification primer 17-2
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1047..1068
;   OTHER INFORMATION: downstream amplification primer 17-2 , complement
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 946..963
;   OTHER INFORMATION: upstream amplification primer 99-4576
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1385..1402
;   OTHER INFORMATION: downstream amplification primer 99-4576 , complement
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1096..1115
;   OTHER INFORMATION: upstream amplification primer 9-19
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1616..1635
;   OTHER INFORMATION: downstream amplification primer 9-19 , complement
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1602..1621
;   OTHER INFORMATION: upstream amplification primer 9-20
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 2074..2093
;   OTHER INFORMATION: downstream amplification primer 9-20 , complement
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 2036..2053
;   OTHER INFORMATION: upstream amplification primer 99-4557
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 2563..2580
;   OTHER INFORMATION: downstream amplification primer 99-4557 , complement
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 2084..2102
;   OTHER INFORMATION: upstream amplification primer 9-1
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 2483..2500
;   OTHER INFORMATION: downstream amplification primer 9-1 , complement
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 2470..2489
;   OTHER INFORMATION: upstream amplification primer 9-21 , complement
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 2062..2081
;   OTHER INFORMATION: downstream amplification primer 9-21
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 3455..3474
;   OTHER INFORMATION: upstream amplification primer 9-3
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 3882..3901
;   OTHER INFORMATION: downstream amplification primer 9-3 , complement
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 3775..3792
;   OTHER INFORMATION: upstream amplification primer 99-4558
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 4336..4356
;   OTHER INFORMATION: downstream amplification primer 99-4558 , complement
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 4902..4920
;   OTHER INFORMATION: upstream amplification primer 99-14419 , complement
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 4444..4463
;   OTHER INFORMATION: downstream amplification primer 99-14419
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 6638..6655
;   OTHER INFORMATION: upstream amplification primer 99-4577
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 7072..7089
;   OTHER INFORMATION: downstream amplification primer 99-4577 , complement
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 7995..8012
;   OTHER INFORMATION: upstream amplification primer 99-4559
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 8576..8593
;   OTHER INFORMATION: downstream amplification primer 99-4559 , complement
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 9622..9639
;   OTHER INFORMATION: upstream amplification primer 99-3148
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 10023..10040
;   OTHER INFORMATION: downstream amplification primer 99-3148 , complement
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 9964..9981
;   OTHER INFORMATION: upstream amplification primer 99-4560
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 10546..10563
;   OTHER INFORMATION: downstream amplification primer 99-4560 , complement
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 10996..11015
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;   OTHER INFORMATION: upstream amplification primer 99-14411 , complement
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 10492..10512
;   OTHER INFORMATION: downstream amplification primer 99-14411
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 11972..11990
;   OTHER INFORMATION: upstream amplification primer 99-4561
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 12481..12501
;   OTHER INFORMATION: downstream amplification primer 99-4561 , complement

  Query Match             1.5%;  Score 44.8;  DB 4;  Length 23187;
  Best Local Similarity   71.6%;  Pred. No. 0.034;
  Matches   73;  Conservative    0;  Mismatches   27;  Indels    2;  Gaps    1;

Qy       1020 TGTTATCCTCAGTGCCTCTCACAATGCCTGGCATATAGTAGTTATTCAGTGACTGT--TT 1077
              || |||||   ||| |||  | | ||||| | | ||||  | || ||||| | | |  ||
Db       9860 TGGTATCCCAGGTGTCTCAAATACTGCCTAGAACATAGGTGGTACTCAGTAATTATTGTT 9919

Qy       1078 CTTGGATGAATGAATGAATGAATAAATAAATGAAGAAATGAA 1119
                 |||||||||||||||||||| ||| ||||||  || |||
Db       9920 GAAGGATGAATGAATGAATGAATGAATGAATGAAAGAAAGAA 9961


RESULT 11
US-09-157-177-118
; Sequence 118, Application US/09157177
; Patent No. 6090558
; GENERAL INFORMATION:
;  APPLICANT: Butler, John M.
;  APPLICANT: Li, Jia
;  APPLICANT: Monforte, Joseph A.
;  APPLICANT: Becker, Christopher H.
;  TITLE OF INVENTION: DNA TYPING BY MASS SPECTROMETRY WITH  POLYMORPHIC DNA
;  TITLE OF INVENTION: REPEAT MARKERS
;  FILE REFERENCE: GETR:017/GETR017P
;  CURRENT APPLICATION NUMBER: US/09/157,177
;  CURRENT FILING DATE: 1998-09-18
;  EARLIER APPLICATION NUMBER: 60/059,415
;  EARLIER FILING DATE: 1997-09-19
;  NUMBER OF SEQ ID NOS: 135
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
;   LENGTH: 300
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-157-177-118

  Query Match             1.5%;  Score 43.8;  DB 3;  Length 300;
  Best Local Similarity   72.2%;  Pred. No. 0.0036;
  Matches   57;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy       1045 GCCTGGCATATAGTAGTTATTCAGTGACTGTTTCTTGGATGAATGAATGAATGAATAAAT 1104
              | |||||| | |  ||  | | || ||    |   || |||||||||||||||||| |||
Db         17 GACTGGCACAGAACAGGCACTTAGGGAACCCTCACTGAATGAATGAATGAATGAATGAAT 76

Qy       1105 AAATGAAGAAATGAATGAA 1123
               ||||||  ||||||||||
Db         77 GAATGAATGAATGAATGAA 95


RESULT 12
US-08-195-744-4
; Sequence 4, Application US/08195744
; Patent No. 5639607
;  GENERAL INFORMATION:
;    APPLICANT:  DESNICK, R.
;    APPLICANT:  WETMUR, J.
;    TITLE OF INVENTION:  METHODS FOR DETERMINING SUSCEPTIBILITY
;    TITLE OF INVENTION:  TO LEAD POISONING
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BRUMBAUGH, GRAVES, DONOHUE AND RAYMOND
;      STREET:  30 ROCKEFELLER PLAZA
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH 720 Kb  STORAGE
;      COMPUTER:  COMPAQ 286e
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/195,744
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  us/07/742,130
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, R., LEHNHARDT, S., DELSIGNORE, M.
;      REGISTRATION NUMBER:  26,154, 33,943, 32,689
;      REFERENCE/DOCKET NUMBER:  28490
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 408-2500
;      TELEFAX:  (212) 765-2519
;      TELEX:  238555
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6063
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  DOUBLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  GENOMIC DNA
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  NO
;    FEATURE:  GENE PRODUCT IS k-AMINO LEVULINATE DEHYDRATASE
;    PUBLICATION INFORMATION:  NONE
US-08-195-744-4

  Query Match             1.5%;  Score 43.8;  DB 1;  Length 6063;
  Best Local Similarity   60.5%;  Pred. No. 0.027;
  Matches   72;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy         1023 TATCCTCAGTGCCTCTCACAATGCCTGGCATATAGTAGTTATTCAGTGACTGTTTCTTGG 1082
                |||| |||| ||||   ||| | | ||||| ||| ||  || ||| | | | ||| ||| 
Db         1538 TATCATCAGGGCCTAGAACAGTACTTGGCACATAATAAGTACTCAATAAATATTTGTTGA 1597

Qy         1083 ATGAATGAATGAATGAATAAATAAATGAAGAAATGAATGAAGAAATAACGTATGGGTGA 1141
                |||||||||| ||  |   |  | ||  |  || |  | | |    ||   |||   ||
Db         1598 ATGAATGAATTAACCACGCATGATATAGATGAAGGCCTAAGGCTCAAAGAGATGATAGA 1656

RESULT 13
US-08-788-279-4
; Sequence 4, Application US/08788279
; Patent No. 5840578
;  GENERAL INFORMATION:
;    APPLICANT:  DESNICK, R.
;    APPLICANT:  WETMUR, J.
;    TITLE OF INVENTION:  METHODS FOR DETERMINING SUSCEPTIBILITY
;    TITLE OF INVENTION:  TO LEAD POISONING
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BRUMBAUGH, GRAVES, DONOHUE AND RAYMOND
;      STREET:  30 ROCKEFELLER PLAZA
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH 720 Kb  STORAGE
;      COMPUTER:  COMPAQ 286e
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/788,279
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/742,130
;      FILING DATE:  07-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, R., LEHNHARDT, S., DELSIGNORE, M.
;      REGISTRATION NUMBER:  26,154, 33,943, 32,689
;      REFERENCE/DOCKET NUMBER:  28490
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 408-2500
;      TELEFAX:  (212) 765-2519
;      TELEX:  238555
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6063
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  DOUBLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:
;      DESCRIPTION:  GENOMIC DNA
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  NO
;    FEATURE:
;      OTHER INFORMATION:  GENE PRODUCT IS k-AMINO LEVULINATE
;      OTHER INFORMATION:  DEHYDRATASE
;    PUBLICATION INFORMATION:  NONE
US-08-788-279-4

  Query Match             1.5%;  Score 43.8;  DB 2;  Length 6063;
  Best Local Similarity   60.5%;  Pred. No. 0.027;
  Matches   72;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy         1023 TATCCTCAGTGCCTCTCACAATGCCTGGCATATAGTAGTTATTCAGTGACTGTTTCTTGG 1082
                |||| |||| ||||   ||| | | ||||| ||| ||  || ||| | | | ||| ||| 
Db         1538 TATCATCAGGGCCTAGAACAGTACTTGGCACATAATAAGTACTCAATAAATATTTGTTGA 1597

Qy         1083 ATGAATGAATGAATGAATAAATAAATGAAGAAATGAATGAAGAAATAACGTATGGGTGA 1141
                |||||||||| ||  |   |  | ||  |  || |  | | |    ||   |||   ||
Db         1598 ATGAATGAATTAACCACGCATGATATAGATGAAGGCCTAAGGCTCAAAGAGATGATAGA 1656

RESULT 14
US-09-369-247-44/c
; Sequence 44, Application US/09369247
; Patent No. 6569992
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 44 Human Secreted Proteins
;  FILE REFERENCE: PZ024P1
;  CURRENT APPLICATION NUMBER: US/09/369,247
;  CURRENT FILING DATE: 1999-08-05
;  EARLIER APPLICATION NUMBER: 60/074,118
;  EARLIER FILING DATE: 1998-02-09
;  EARLIER APPLICATION NUMBER: 60/074,157
;  EARLIER FILING DATE: 1998-02-09
;  EARLIER APPLICATION NUMBER: 60/074,137
;  EARLIER FILING DATE: 1998-02-09
;  EARLIER APPLICATION NUMBER: 60/074,341
;  EARLIER FILING DATE: 1998-02-09
;  EARLIER APPLICATION NUMBER: 60/074,141
;  EARLIER FILING DATE: 1998-02-09
;  NUMBER OF SEQ ID NOS: 172
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
;   LENGTH: 819
;   TYPE: DNA
;   ORGANISM: Homo sapiens
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US-09-369-247-44

  Query Match             1.4%;  Score 43.2;  DB 4;  Length 819;
  Best Local Similarity   65.6%;  Pred. No. 0.011;
  Matches   63;  Conservative    0;  Mismatches   33;  Indels    0;  Gaps    0;

Qy       1025 TCCTCAGTGCCTCTCACAATGCCTGGCATATAGTAGTTATTCAGTGACTGTTTCTTGGAT 1084
              |||  ||   || |  ||  |||||||| |||  ||  | |||   | | ||||| ||| ||
Db        252 TCCCTAGCATCTATGGCAGGGCCTGGCACATAAAAGGCAATCAAAAAATGTTTGTTGAAT 193

Qy       1085 GAATGAATGAATGAATAAATAAATGAAGAAATGAAT 1120
               ||||||||||||| | ||| |   || |||  | |
Db        192 AAATGAATGAATGAGTGAATGAGCCAACAAAACACT 157


RESULT 15
US-09-205-258-13/c
; Sequence 13, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
;  APPLICANT: Young et al.
;  TITLE OF INVENTION: 207 Human Secreted Proteins
;  FILE REFERENCE: PZ007P1
;  CURRENT APPLICATION NUMBER: US/09/205,258
;  CURRENT FILING DATE: 1998-12-04
;  EARLIER APPLICATION NUMBER: PCT/US98/11422
;  EARLIER FILING DATE: 1998-06-04
;  EARLIER APPLICATION NUMBER: 60/048,885
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US-09-205-258-13

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